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Sequence 121728, Sequence 22737, A Sequence 115236, Sequence 2, Appli Sequence 121731, Sequence 121731, Sequence 128071, Sequence 128071, Sequence 128028, Sequence 128028, Sequence 22734, A Se
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'cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep: *

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US-09-968-561A-2

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US-09-791-537-121731

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US-09-791-537-121728

US-09-791-537-121728

US-09-791-537-121728, Application US/09791537

SEQUENCE 121728, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Blonomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY I

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 121728

LENGTH: 244
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; Sequence 22737, Application US/09791537
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Matches 194; Conser
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Pred. No. 2.6e-52;
5; Mismatches 27;
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(Sequence 2, Application US/09511939

(GENERAL INFORMATION:

APPLICANT: Tomlinson, Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage D.

FILE REFERENCE: 8039/1070

CURRENT APPLICATION NUMBER: US/09/511,939

CURRENT FILING DATE: 2002-04-10

PRIOR FILING DATE: 1997-10-20

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 350

SOFTWARE: PATENTIN VERSION 3.1
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Best Local Similarity 80.6%;
Matches 195; Conservative
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SOFTWARE: Pack
SEQ ID NO 2
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           APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: HETHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22737
LENGTH: 240
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GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 115236

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   GENERAL INFORMATION;
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US-09-791-537-115236
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; ORGANISM: Homo :
US-09-791-537-22737
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 115235
LENGTH: 248
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20; Mismatches
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US-09-791-537-115235
; Sequence 115235, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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Best Local Similarity 74.9%;
Matches 185; Conservative
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US-10-127-890-148
; Sequence 148, Application US
; GENERAL INFORMATION:
APPLICANT: Better, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: synthetic US-09-791-537-115235
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GTKLEIK
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                 Display
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                                                                                                                                                                                                                                                                                                                         Score 992; DB 5;
Pred. No. 2.6e-52;
16; Mismatches 2;
APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Di
FILE REFERENCE: 8039/1073B

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: GB 9722131.1

PRIOR FILING DATE: 1997-10-20

PRIOR APPLICATION NUMBER: US 60/065,248

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: PCT/GB98/03135

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 350

SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-791-537-121731
; Sequence 121731, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TILE OF INVENTION: METHODS OF USE THER
; TILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,53
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 121731
; LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 LLIYAASSLQSGVPSRFSGSGSGTDFTLTI
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CRGANISM: Homo sapiens
US-09-968-561A-2
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US-09-791-537-121731
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Best Local Similarity
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LENGTH: 240
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Best Local S:
Matches 187,
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               Studnika, Gary M.
INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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                                                                                                                                                                                 ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
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                                                                                                  d & Malloy, Ltd.
Street, 34th floor
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d. No. 6.5e-47;
Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                            US94/05348
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                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held
STREET: 500 West Madison S
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.1%; Pred Matches 169; Conservative 33; M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID
US-10-127-890-148
                                               Proteins
Stephen
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SEQUENCE CHARACTERISTICS:
                                                                  NUMBER OF SEQUENCES: 173
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Carroll,
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                                 TITLE
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 34222
LENGTH: 243
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 128071
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Pred. No. 3.6e-46;
                                                                                                                        RESULT
US-09-791-537-34222
Sequence 34222, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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74.0%;
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US-09-791-537-128071
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Best Local Similarity
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US-09-791-537-128071
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                                                                                                                                                                                                                                                                                  Length
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PRC
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 9775
LENGTH: 243
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69.2%; Pred. No. 9.5e-46;
ive 30; Mismatches 42
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Pred. No. 5.9e-46,
30; Mismatches 46
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Sequence 18026, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 18026
LENGTH: 243
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Best Local Similarity 68.2%;
Matches 165; Conservative 3
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Best Local Similarity
Matches 166; Conser
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US-09-791-537-18026
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|LSASVGDRVTITCRASQGISSWLAWYQQKP
                                                                                               1 QVQLVQSGGGVVQPGRSLRLSCAEGGFTFSSYSMHWVRQAPGKGLEWVAVM-WFDGTEKY
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                                  QVRLQQSGGLVQPGRS1RLSCAASGFTFDDYAMHWVRQAPGKGLEWVSCMTWNSGSIGY
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No. 5.3e-46;
smatches 27;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 128029, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THER
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 128029
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US-09-791-537-9775
; Sequence 9775, Application US/09791537
; GENERAL INFORMATION:
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  Conservative
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US-09-791-537-128029
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225 GTKLEIK 231
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; TYPE: PRT
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Sequence 128028
Sequence 128028, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Dece, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 128028
LENGTH: 232
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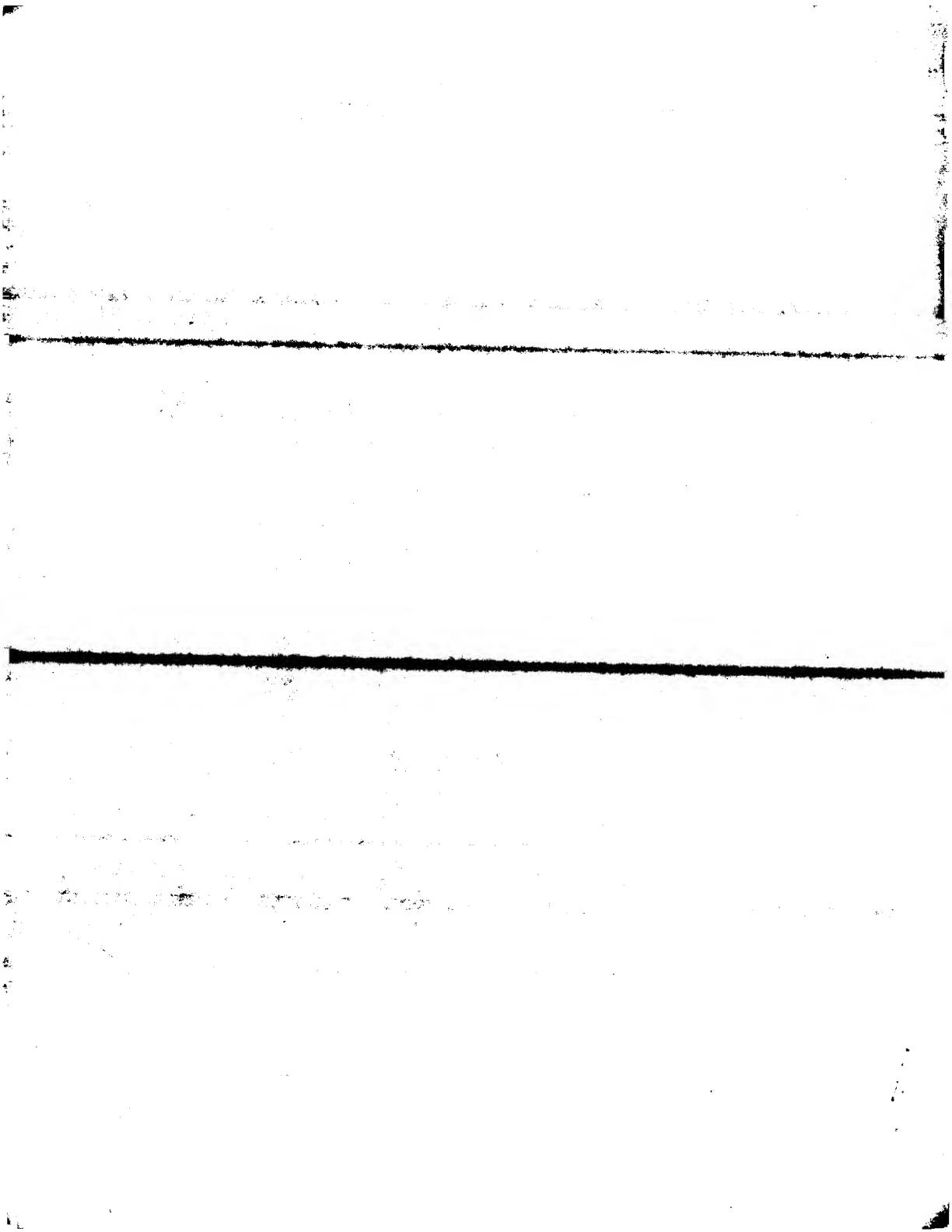
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: 3.0

CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0

SEQ ID NO 22734

LENGTH: 2.44
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Pred. No. 1.2e-45;
23; Mismatches 28
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Best Local Similarity 70,4%; Pred.
Matches 174; Conservative 23; Mis
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| 225 GTKLEIK 231
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|QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEWMGWIDPNNGDTRF
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 Length 244;
                        Indels
                 40;
Score 878; DB 5; Pred. No. 1.7e-45
Query Match 68.7%;
Best Local Similarity 66.3%;
Matches 161; Conservative
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version
- 2000
 GenCore
Copyright (c) 1993
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Search time 39.61 Seconds (without alignments) 148.613 Million cell updates/secCQQLISYPLTFGGGTKVEIK 241 ٠. OM protein - protein search, using sw model August 15, 2002, 16:22:15 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-779-457-50 1278 1 QVRLQQSGGGLVQPGRSLRL. Perfect score: Scoring table: Sequence: Run on: Title:

231628 hits satisfying chosen parameters: Total number of

231628 segs, 24425594 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

ies Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summar. Issued_Patents_AA:*
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5: /cgn2_6/ptodata/2/laa/FUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

Description	Sequence 75, Appl Sequence 76, Appl Sequence 77, Appl Sequence 148, App Sequence 148, App Sequence 148, App Sequence 148, App Sequence 148, Appl Sequence 2, Appli Sequence 14, Appl Sequence 16, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 25, Appl
SUMMARIES	US-08-918-148-75 US-08-918-148-75 US-08-918-148-76 US-08-918-148-77 US-08-918-148-77 US-08-918-148-77 US-08-488-113B-148 US-08-46-360-148 US-08-646-360-148 US-09-136-389-148 US-09-136-389-148 US-09-136-389-14 US-09-136-389-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-109-207C-22 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-109-207C-23 US-09-553-498-8
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Length	20000000000000000000000000000000000000
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Sequence 1, Appli	Sedneuce 72, Appl	Sequence 34, Appl	Sequence 34, Appl	Sequence 34, Appl	Sequence 34, Appl	Sequence 9, Appl1	Sequence 11, Appl	Sequence 109, App	Sequence 11, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 85, Appl	Sequence 90, Appl	Sequence 18, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 7, Appli
US-07-843-125-1	US-U8-956-U4/-Z5	US-09-227-693-34	US-08-331-398A-34	US-08-331-397B-34	US-08-759-804A-34	0-620-010-00-00	US-09-079-029-11	US-08-646-265A-109	US-07-843-125-11	US-08-564-164A-4	US-09-485-737B-2	US-09-485-737B-85	US-09-485-737B-90	US-08-553-497A-18	US-08-235-838-14	US-08-465-473B-14	US-08-235-838-7
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63.3	0. to	62.0	62.0	62.0	62.0	61.3	61.3	61.3	61.0	8.09	60.2	60.2	60.2	59.9	59.6	59.6	59.6
808.5	308 508	792.5	792.5	792.5	792.5	784	783.5	783	779.5	777	769.5	769.5	769.5	166	762	762	762
28	7	30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45

ALIGNMENTS

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KESULT 1
US-08-918-148-75
Sequence 75, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Garter, Paul J.
APPLICANT: Garner, Paul J.
APPLICANT:
```

Gaps 181 LIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVEI 1; Length 245; Indels DB 4; 26; 79.1%; Score 1010.5; DB ilarity 79.3%; Pred. No. 3.6e-72 Conservative 23; Mismatches 2 Query Match Best Local Similarity Matches 191; Conser 182 ద g Op

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RESULT 2 US-08-918-148-78 ; Sequence 78, Application US/08918148A

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US-08-918-148-77
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                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                      63 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRGST-GMDVWGRGTLVTVSSG
                                                                                                                                                                                                                                                                                                            'DDY AMHWVRQAPGKGLEWVSCMTWNSGSIGY
                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSLQPEDFGTYYCOQLISYPLTFGGGTKVEI
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. No. 1.5e-71;
ismatches 27;
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.3e-70;
as 29;
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No. 2.3e
ismatches
                                                                                                8,148A
                                                                                                                                                                                       ; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 78
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 76, Application US/08918148A; Patent No. 6342220; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W. Carter, Paul J.
APPLICANT: Fendly, Brian M.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979;
CURRENT FILING DATE: 1997-08-25;
CURRENT FILING DATE: 1997-08-25
                                                                                                                                                                                                                                                               Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                    122 GGGSGGGSGGGSKIQMTQSPSTLSASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 LIYAASTLQSGVPSRFSGSGSGTEFTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.4%; 5c.
79.3%; Pre
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 79.3
Matches 191; Conservative
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; ORGANISM: artificial
US-08-918-148-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 76
LENGTH: 245
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Best Local S
Matches 185
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ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
                                                                                                              GGGPGGGGGGGGSDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVEI
                                                                                                                                                                                       ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
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US-08-564-164A-2
; Sequence 2, Application US/08564164A
; Patent No. 6159947
; GENERAL INFORMATION:
; APPLICANT: Schweighoffer, Fabien
; APPLICANT: Tocque, Bruno
; TITLE OF INVENTION: Intracellular Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 987; DB 4;
Pred. No. 2.5e-70;
25; Mismatches 28
                                                                                                                                                                                                                                                             Sequence 77, Application US/08918148A; Sequence 77, Application US/08918148A; Patent No. 6342220; GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Fendly, Brian M.
APPLICANT: Fendly, Brian M.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.2%;
Matches 186; Conservative 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 77
LENGTH: 244
TYPE: PRT
ORGANISM: artificial
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and Use

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.5%;
Best Local Similarity 70.1%;
Matches 169; Conservative 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
TITLE OF INVENTION: Imm
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANGREWS,
STREET: 500 West Madis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-EPHNTDAFDIWGRGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                             Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               939.5;
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/FR94/00714 FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 93/07241 FILING DATE: 16-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                    STATE.

COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164A
TITNG DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO.
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Sequence 148, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                    ADDRESSEE: Rhone-Poulenc Rorer InstrEET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Savitzky, Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST93030-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.5%; Score ilarity 72.7%; Pred. Conservative 29; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (610)454-3816
(610)454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-564-164A-2
                                                                                                                                                                                                                                                           FILING DATE: 28-DEC-CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                      NUMBER OF SEQUENCES: 1'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 IK 241
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Proteins
169
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                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-9155
FILEPHONE: 312/707-9155
FILEPHONE: 312/707-9155
                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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Pred. No. 1.2e-63;
33; Mismatches 38
                     STREET: 500 West Madison Street, 34th floor CITY: Chicago STATE: Illinois COUNTRY: USA
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ij

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Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: US 07/901,707
FILING DATE: US 07/901,707
FILING DATE: US 07/707 E77
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. No. 1.2e-63;
ismatches 38;
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                        Sequence 148, Application US/08477484B Patent No. 5756699 GENERAL INFORMATION:
                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Crafte OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,918
ER: 11022US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.5%; Score ilarity 70.1%; Pred. Conservative 33; Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/787,5 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
  2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 1102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 amino acids
amino acid
 16:32:47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-148
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INFORMATION FOR SEQ ID N
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Best Local Similarity
Matches 169; Conser
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US-08-477-484B-148
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GGGPGGGGGGGGGDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL 180
                                                                                  Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                  Sequence 148, Application US/08646360

Sequence 148, Application US/08646360

Patent No. 5837491

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribo
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBER: US/08/646,360
13-MAY-1996
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amino acid
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; MOLECULE TYPE: protein
US-08-646-360-148
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US-08-646-360-148
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STATE: 1
COUNTRY:
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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndress
                                                                                                                                ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
                                                          QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY
    240;
    Length
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
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                                38;
  901.5; DB 2
No. 1.2e-63;
                               Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: US 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 West Madison Street,
                                                                                                                                 70.5%; Score 70.1%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 148, Application US/08839765 Patent No. 6146631 GENERAL INFORMATION:
                             33;
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TELEPHONE: 312/707-8889
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                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
Query Match
Best Local Similarity
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                             169;
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                                Matches
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ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG 120 GGGPGGGGGGGGDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL 180 Comprising Ribosome-Inactivating 181 LIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVEI QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGS1GY 1; Length 240, Indels APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Rib
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA Version #1.25 38; DB 4; Score 901.5; DB 4 Pred. No. 1.2e-63; 33; Mismatches 38 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 PRIOR APPLICATION DATA: US 07/988,430 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 Sequence 148, Application US/09136389 Patent No. 6146850 GENERAL INFORMATION: 08/646,360 ; TELEFAX: 312/707-9155 ; TELEX: 650 388-1248 ; INFORMATION FOR SEQ ID NO: 14 ; SEQUENCE CHARACTERISTICS: ; LENGTH: 240 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-839-765-148 70.5%; 70.1%; 13-MAY-1996 Conservative CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-MAY-PRIOR APPLICATION DATA: APPLICATION NUMBER: Query Match Best Local Similarity Matches 169; Conser 60661 US-09-136-389-148 K 240 K 241

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TOPOLOGY: 1
MOLECULE TYPE:
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Matches 166;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTNYGMNWVRQAPGKGLEWMGWINTHTGEPTY
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hes 38;
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US-07-958-140-2
Sequence 2, Application US/07958140
Patent No. 5489525
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tow
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.O
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|. No. 1.2e
|ismatches
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     0.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94105-1492
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/958,140
TILING DATE: 19921008
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                              33; M1
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Best Local Similarity 70.1%; Pred.
Matches 169; Conservative 33; Mi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LIYRANRLESGVPSRFSGSGSGTDYTLT
                                                                                                                                                                                                                                                                                   LENGTH: 240 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                             TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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STATE:
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122 GGPGGGGGGGGSDVVMTQSPSFLSAFVGDTITTTCRASQGIYNYLAWYQQKPGKAPKLL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETILORY OF THE PROBLEM OF CYTUS9309166

GENERAL INFORMATION:

APPLICANT: Pastan, Ira H.

ITILE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend

STREET: One Market plaza, Steuart Street Tower

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94105-1492

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATION:

MEDIUM TYPE: PatentIn Release #1.0, Version #1.25

CLASSIFICATION NUMBER: PCT/US93/09166

FILING DATE:

ATTORNEY/GENT INFORMATION:

NAME: PATENDENCE/DCKET NUMBER: 15.280-77

TELECOMMUTICATION INFORMATION:

TELEFRAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 2:

SECURATE CHARACTERIFER CATER
                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                Score 882; DB 1;
Pred. No. 4.1e-62;
); Mismatches 42
                  NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                69.0%; Scilarity 69.2%; Pr
Conservative 30;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE; protein US-07-958-140-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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2 VRLQQSGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGYA 61
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                                             21
                                                                                                       81
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                                            Length 243;
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
                                                                       42;
                                         , rred. No. 4.1e-62;
30; Mismatches 42.
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REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,1
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 DSVKGRFTISRDNAKNSLYLQMNSLRAEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 69.6%; Pred.
Conservative 27; Mis
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08661052
Patent No. 5837243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                         Ouery Match
Best Local Similarity 69.2%;
Matches 166; Conservative 3
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Joel Goldstein
Robert Graziano
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amino acid
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Best Local Similarity
Matches 172; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwa
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US-08-661-052-14
PCT-US93-09166-2
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APPLICANT:
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                                                                      DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTD-AFDIWGRGTLVTVSSG
                                                                                                                                                                Length 301;
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APPLICANT: Joel Goldstein
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09/188,082
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09188082 Patent No. 6270765 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6-
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 172; Conser
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260 GTKVEIK 266
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US-09-188-082-14
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                                                                                                                                                                             GKAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGG 234
 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTD-AFDIWGRGTLVTVSSG
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APPLICANT: Joel Goldstein
APPLICANT: Joel Goldstein
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massach...
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
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40;
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. No. 1.8e-61;
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REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043C
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (617)227-7400
TELEFRAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,
APPLICATION NUMBER: US 08/484,
APPLICATION NUMBER: US 08/484,
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                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
201 GKAPKLLIYWASTRESGVPSRFSGSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUNE-1999: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 69.6
Matches 172; Conservative
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. USA
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US-08-661-052-16
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US-08-661-052-16
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GTKVEIK 266
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

1: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

4: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

5: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*

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6: SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*

7: SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*

8: SIDSI/gcgdata/hold-geneseqy-embl/AA1991.DAT:*

7: SIDSI/gcgdata/hold-geneseqy-embl/AA1991.DAT:*

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ALIGNMENTS

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Human; WSX receptor; clone #17; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                Matthews W;
                                                                                 Human WSX receptor agonist antibody clone #17
                                                                                                                                                                                                                                                                                                                                                                 Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                Chiang NY,
          AAW24063 standard; Protein; 241
                                                                                                                                                                                                                                                                              97WO-US00325.
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96US-0585005
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Carter PJ,
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08-JAN-1996;
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                                 AAW24063;
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AAW24063
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Best_Local Similarity
Matches 200; Conserv
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12-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                            receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor antibody can be used as an agonist differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal.
                                                                                                                                                                                                                                                                                                                                                 QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marker; cancer; drug targetting;
cific; internalisation; non-immunogenic.
                                                                                                                                         especially a human, is suffering from decreased blood cell lineages. This is useful when a mammal, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to repopulate e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertrigilveriation, insulin and cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to develop
                                                                                                                                                                                                                                                                                                          Length 241;
                   WSX receptor and related antibodies and ligands - used products for diagnosis and therapy, e.g. for improving haematopoiesis or for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor antibody scFv Cl
                                                                                                                                                                                                                                                                                                          Score 1278; DB 18;
Pred. No. 1.1e-78;
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                                                            English
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                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNAKNSLYLQMNSLRAE
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31..35
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                                                            Example 14; Pages 122-123;
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                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 241; Conser
                                                                                                                                                                                                                                                                             241 AA;
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Homo sapiens
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as vinblastine, vindesine or melphalan; ribozymes; or antisense as vinblastine, vindesine or melphalan; ribozymes; or antisense molecules. The antibodies may also be used for in vivo or in vitro detection and/or quantitation of the c-erb-2 receptor and thus diagnosis and/or localisation of cancers characterised by expression of c-erb-2. Although antibodies have previously been used to target tumour cells, then hampered by the paucity of tumour specific antibodies has been limited. The utility of prior art antibody immunogenicity, low binding affinity, and poor tumour penetration. Immunogenicity could be avoided and toxicity reduced if high affinity tumour specific human antibodies were available. However, the production of human monoclonal antibodies using conventional hybridoma technology has proven difficult. Also, most of the antibodies produced react with antigens that are also common to non-malignant cells, which makes them unsuitable for use as tumour-targetting molecules. The antibodies of the invention overcome these difficulties, as they are targetted to a function of immunogenicity as they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an internalising humanised antibody, scFv Cl, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/meu oncogene. The scFv Cl antibody binds to the epitope of the c-erbB-2 receptor that is bound by Cl antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor, the protein which is overexpressed by 30-50% of breast carcinomas and other adenocarcinomas, and thus provides a useful cell surface marker for specifically targetting tumour cells. The antibodies of the invention are used as tumour-targetting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin; radionuclides; ligands such as growth factors; therapeutic agents such as ricin, abrin or Pseudomonas exotoxin; such as ricin, ariches; therapeutic agents such
"Heavy chain variable region (VH) complementarity determining region. 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                          'Light chain variable region (VL) complementarity determining region 1 (CDR1)"
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larity 83.0%; Pred. No. 1.1e-62;
Conservative 15; Mismatches 26;
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                                                                                                                   "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "VL-CDR2"
223..231
/note= "VL-CDR3"
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/note= "VH-CDR3"
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                                                                                                                                                                                             "VH-CDR2
                                                                                                                                                                                                                                                                                                                                                    /note- "Light
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99US-0250056.
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N-PSDB; AA255615.
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                                                   GGGPGGGGGGGGSDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKL
                                                         virus; AIDS;
                                                                                                                                                                                                    mmunodeficiency
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/label= CDR_1_heavy_chain
37..50
/label= Framework_2_heavy_chain
51..67
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/label= CDR_2_heavy_chain
68..99
/label= Framework_3_heavy_chain
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/label= Framework_1_

166..176

/label= CDR_1_light_(

177..191

/label= Framework_2_1-

192..203

/label= CDR
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/label= CDR_3_light_c
243..253
/label= Framework_4_
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32..36
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                                                          Recombinant sc3D6 anti-HIV gp160 an
                                                                                                                                                 AAR20059 standard; Protein; 248 AA.
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/label- linker
143.165
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/label = Cr
117
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Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC; megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                         113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The cell line 3D6 (87110301; Porton Down) produces a MAb of the IgG1/kappa type that reacts specifically with HIV-1 gp41 and also weakly cross-reacts with HIV-1 gp120. Gene construct sc3D6 was engineered using the variable region coding regions of the heavy and light chains of antibody 3D6, joined by a linker. The recombinant protein binds to HIV gp160. See also AAQ20066 and AAQ20067.
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                                                                                                                                                                                                                                                                                                                                         Length 248;
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თ
                                                                                                                                Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
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22;
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                                                                       Kohl
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larity 79.4%;
Conservative 2
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91WO-1000067
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                                                                       Himmler
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Best Local Similarity
Matches 197; Conserv
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240 pgtkvdik
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                        29-MAY-1990;
                                                                       Felgenhauer
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thrombopoletin receptor (TPO-R). The antibodies which bind the TPO-R can be used in the same way and for the same indications as thrombopoletin to the same way and for the same indications or growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating increase platelet production. They can be used for treating immunological or hematopoletic disorders, especially thrombocytopenia.

Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia following chemotherapy or bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia, congenital thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for the treatment of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablative chemotherapy for the constant of solid tumours or leukaemia, myeloablatical chemotherapy for the constant of solid tumours or leukaemia.
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79.38;
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The invention relates to an agonist antibody (Ab) which binds to a thrombopoletin receptor (TPO-R). The antibodies which bind the TPO-R can thrombopoletin receptor (TPO-R). The antibodies which bind the TPO-R can be used in the same way and for the same indications as thrombopoletin can expect the same indications as thrombopoletin of growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoletic disorders, especially thrombocytopenia. Thrombocytopenia -associated bone marrow transplant of a plastic anemia following chemotherapy or bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia, congenital thrombocytopenia, thrombocytopenia and minune thrombocytopenia, thrombocytopenia and myelodysplasia. They can also be used in e.g. myelodysplasia, and immune thrombocytopenia, myelodysplasia, myelodysplasia, thrombocytopenia, myelodysplasia, diopathic aplastic anemia, congenital thrombocytopenia, and immune thrombocytopenia. The antibodies which bind to the MuSK receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The sequences AAYOG713-YOG718 represent single chain FV (SCFV) fragments of
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                                                                                                       Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC; megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour;, MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
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larity 79.7%; Pred. No. 1.2e-60;
Conservative 22; Mismatches 26; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New thrombopoietin receptor agonist antibodies -
treating immunological or hematological disorders
                                                                        Antibody 12B5 single chain Fv (scFv) fragment.
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les 192; Conser
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                     PIGR; ligand; therapeutic;
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                                                                                                                        Amino acid sequence of secreted form of scFv
                                                                                                                                  Polymeric immunoglobulin receptor; pIgR; carcinoma diagnosis; veterinary; scFv 4A.
                                                                                                                                                                           23..27
/note= "FLAG epitope"
28..58
                                                                                                                                                                                                                                                                /note= "linker"
163..185
/note= "light chain 1
186..196
/note= "CDRI"
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/note= "light chain f
274..283
/note= "myc epitope t
288..293
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140..147
/note- "Heavy chain
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/note- "light chain
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251..259
/note= "CDR3"
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/note= "PelB leader
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                    AAG65715 standard; protein; 293 AA
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148.162
-+a= "linker"
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/note- "CDR2"
94..125
/note- "Heavy c'
126..139
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/note- "CDR2"
219..250
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/note=
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/note-
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The invention provides ligands that bind specifically to a region of an animal cell polymeric immunoglobulin receptor (pigR). The pigR cleaves to produce a stalk region remaining attached to the cell and a secretory component existing in the organ of interest in several forms. The ligands of once bind to the stalk or the most abundant form of the secretory component present in the organ under physiological conditions. The ligands are useful for transporting therapeutic or diagnostic compositions into or across cells expressing pigR, useful to introduce or transport ligands such as antibodies and/or to deliver biologically active components such as proteins, nucleic acids or detectable labels. They are used to deliver therapeutic compositions to mucosal surfaces such as the gastro-intestinal tract, respiratory system etc. in humans. They are also useful to label cells expressing pigR, e.g. to distinguish epithelial cells from a mixed cell population in pathology studies or to aid in carcinoma diagnosis (since pigR expression is reduced in carcinomas relative to normal epithelium). They can also be used to deliver veterinary compositions, especially in mammals such as farm, domestic or wild mammals or birds reared for human consumption. The present sequence represents the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                          New ligands binding to a specific region of a polymeric immunoglobulin receptor, useful for transporting therapeutic or diagnostic compositions into or across cells expressing pIGR e.g. in drug delivery
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Pred. No. 1.7e-59;
19; Mismatches 30;
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Best Local Similarity 79.3%;
Matches 192; Conservative 19
                                                            2000US-192197P
2000US-192198P
26-MAR-2001; 2001WO-US09699
                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                 Chapin SJ,
                                                                                                                                                                                                                                                                                             WPI; 2001-611619/70
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                                                            27-MAR-2000;
27-MAR-2000;
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AAY02472;

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Query Match
Best Local Similarity
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             AAB46044
                                                  The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in diagnostic, prophylactic and therapeutic procedures. The present sequence represents the single chain antibody (SCFV) that forms the seguence represents according to the invention.
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                                                 ligand; non-functional;
ScFv.
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No. 1.8e-59;
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                                                                                                                                                                                                                                                                                                                         Screening for functional polypept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening; functional polypeptide enrichment; single chain antibody.
                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2; 67pp; English,
                        A single chain antibody (ScFv).
                                                                                                                                                                                    97GB-0022131.
97GB-0062131.
97US-0065428.
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                                                                                                                                                             98WO-GB03135
 (first entry)
                                                                                                                                                                                                                                                               Winter
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                                                                                      Unidentified
                                                                                                            W09920749-A1
                                                                                                                                                                                     21-NOV-1997;
                                                                                                                                                             20-0CT-1998;
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13-NOV-1997;
15-JUL-1999
                                                                                                                                     29-APR-1999
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Matches 195
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This invention describes a novel vaccine (VI) against

conformation-dependent antigens (CDA) comprising DNA (I) and/or an

antibody, or peptide which immunologically imitates CDA, is new. (I)

cancedes a region of an antidiatypic antibody (Ab2) or another peptide

which: (a) specifically binds to the binding site of an antibody (Ab1)

conformation binding molecule; and (b) immunologically minates the

initial antigen binding molecule; and (b) immunologically minates the

conformation-dependent, and has an immunogenic structure defined by a

specific spatial conformation of amino acids. (I) is used in the form

of linear or circular naked DNA and/or with a viral vector and/or

adjuvants. The products of the invention have cytostatic, virucidal,

of linear or circular naked DNA and/or with a viral vector and/or

adjuvants. The products of the invention have cytostatic, virucidal,

antibacterial and antiparasitic. The invention also describes (I) a

corresponding vaccine (V2) against antigens which are not proteins or

peptides, as defined above but which have epitopes which show an

immunogenic structure; (2) preparing (V1) and (V2); (3) human

antidiotypic antibody fragments against the MUC1-conformation epitope

having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (5) antidiotypic amino acid sequences, all fully defined in the specification; (6) antidiotypic amino acid sequences, all fully defined in the specification; (6) residue amino acid sequences, all fully defined in the specification; (6) residue amino acid sequences, all fully defined in the specification; (6) residue amino acid sequences, all fully defined in the specification; (6) residue amino acid sequences, all fully defined in the specification; (6) residue amino acid sequences, all fully defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat

cancer, and infectious diseases, effective in cases where vaccination has

previously not been possible.
                                                                                                                                                                                                                                                                                                                                                                                       MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease.
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                                                                                                                                                                                                                                                                                                    Human TF anti-idiotype antibody fragment
AAB46044 standard; Peptide; 240 AA
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99DE-1043016
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09-SEP-1999;
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Length 240;

Score 988; DB 22; Pred. No. 3.3e-59;

77.3%; 79.8%;

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Carter PJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lependent antigen; antibody; cancer;
virucidal; antibacterial; TF antige
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                               QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY
                                          evgllesggglvqpggslrlscaasgftfssyamswvrqapgkglewvsaiqwsgestwy
                                                                                                                                              BDTITITCRASQGIYNYLAWYQQKPGKAPK
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 Mismatches
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                                                                                                                                               GGGPGGGGGGGG - DVVMTQSPSFLSAFVC
                                                                                     AAB46045 standard; Peptide; 240 AA.
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99DE-1043016.
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 Conservative
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09-SEP-1999;
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Matches
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peptides, as defined above but which have epitopes which show an antidotypic antibody fragments against the MC1-conformation epitope antidotypic antibody fragments against the MC1-conformation epitope having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope mimics having one of 16 9-17 residue amino acid sequences, all fully in the specification; (5) antidiotypic antibody fragments against the TF antigen having one of 24 approximately 200 residue amino acid sequences, clully defined in the specification; (6) TF carbohydrate epitope mimetics having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics acid specification; and (7) DNA sequences encoding the fragments and derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasites. The vaccines are effective in cases where vaccination has
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3.3e-59;
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Mismatches
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Gurney AL;

Fendly BM,

us-08-779-457-50.rag

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The invention relates to an agonist antibody (Ab) which binds to a thrombopoletin receptor (TPO-R). The antibodies which bind the TPO-R can be used in the same way and for the same indications as thrombopoletin or growth of case increase platelet production. They can be used for treating megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoletic disorders, especially thrombocytopenia. Thrombocytopenia - associated bone marrow transplant) may be effectively created with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia, congenital thrombocytopenia, thrombocytopenia in thrombocytopenia, thrombocytopenia, myelodysplasia. They can also be used in e.g. myelodysplasia.

CHIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia, congenital thrombocytopenia, thrombocytopenia, myelodysplasia. They can also be used in e.g. myelodysplasia.

CHIV-induced and non HIV-induced), chronic idiopathic chemotherapy for myelodysplasia. They can also be used in e.g. myelodysplasia.

CHIV-induced and non HIV-induced in e.g. myelodysplasia.

CHIV-induced and non HIV-induced, thrombocytopenia and immune chrombocytopenia. The antibodies which bind to the MuSK receptor can be used for improving neuromuscular induction in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The sequences AAYO6713-Y06718 represent single chain FV (SCFV) fragments of
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nerapy; leukaemia; tumour;, MuSK; CDR;
complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eceptor; TPO-R; thrombopoietin; DIC;
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sslqpddfatyycqqysnypltfgggtklei
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                                                        for
                                                       useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         987.5; DB Zu;
No. 3.7e-59;
-haq 29;
                                                       st antibodies -
ogical disorders
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                                                        agonia
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                                                                         or hematold
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                                                                                                            Disclosure, Fig 1; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                   thrombopoietin receptor
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                  WPI; 1999-204666/17
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Matches 185; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA;
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                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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thrombopoletin receptor (TPO-R). The antibodies which binds to a thrombopoletin receptor (TPO-R). The antibodies which bind the TPO-R can be used in the same way and for the same indications as thrombopoletin can stimulate proliferation, differentiation or growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoletic disorders, especially thrombocytopenia. Thrombocytopenia -associated bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia and congenital thrombocytopenia, thrombocytopenia and myelodysplasia. They can also be used in e.g. myelodysplasia, antipogeneic bone marrow transplant, myelodysplasia, chemotherapy for autologous or allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic anemia, congenital thrombocytopenia, and immune thrombocytopenia. The mutbhodies which bind to the Musk receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The sequences AAVO6713 represent single chain FV (scFV) fragments of various antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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(1)
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                                                                                                                                                                                                                                              New thrombopoietin receptor agonist antibodies - treating immunological or hematological disorders
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ilarity 77.2%; Pred. No. 3.9e-59; 
Conservative 25; Mismatches 28;
                                                                                                                                                                               Gurney
                                                                                                                                                                               BM,
                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 86pp; English.
                                                                                                                                                                              Fendly
                                                                               98WO-US17364
                                                                                                              97US-0918148
                                                                                                                                                                                  PJ,
                                                                                                                                                (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             various antibodies
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              WO9910494-A2
                                                                               21-AUG-1998;
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                                                04-MAR-1999
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Matches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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This invention describes a novel vaccine (VI) against conformation-dependent antigens (CDA) comprising DNA (I) and/or an antibody, or peptide which immunologically initates CDA, is new. (I) encodes a region of an antidotypic antibody (Abb) or another peptide which: (a) specifically binds to the binding site of an antibody (Abl) or an antigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form of linear or circular naked DNA and/or with a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (I) a corresponding vaccine (V2) against antigens which are not proteins or immunogenic structure; (2) preparing (V1) and (V2); (3) human corresponding vaccine (V2) against the MUC1-conformation epitope mimics antidiotypic antibody fragments against the MUC1-conformation epitope mimics (autily defined in the specification; (4) MUC1-conformation epitope mimics specification; (5) antidiotyphic antibody fragment against the TE specification; (5) artidiotyphic antibody fragment epitope mimics the specification; (6) TF carbohydrate epitope mimetics having one of 16 9-17 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics having one of 27 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics having one of 27 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasitles. The vaccines are effective in cases where vaccination has previously, not been neasing
                                                                                                                                                                                                 ependent antigen; antibody; cancer; virucidal; antibacterial; TF antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccines against conformation-dependent or non-peptide antigens, based on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                  Human TF anti-idiotype antibody fragment
                                                                                                                                                                                           MUC1; human; vaccine; conformation-dantiidiotypic antibody; cytostatic; antiparasitic; infectious disease.
                      AAB46040 standard; Peptide; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 11; 36pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     previously not been possible.
                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-DE01809.
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99DE-1043016
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                            WO200073430-A2.
                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2000;
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09-SEP-1999;
                                                                                                         23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goletz S,
                                                                AAB46040;
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AAB46040
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Query Match
    77.1%; Score 985; DB 22; Length 240;
Best Local Similarity 79.8%; Pred. No. 5.3e-59;
Matches 193; Conservative 16; Mismatches 29; Indels 4; Gaps 2;
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This invention describes a novel vaccine (VI) against conformation-dependent antigens (CDA) comprising DNA (I) and/or an antibody, or peptide which immunologically imitates CDA, is new. (I) encodes a region of an antidiotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an antigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form of linear or circular naked DNA and/or with a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) human immunogenic structure; (2) preparing the MUC1-conformation epitope MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antiidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease. based GGGPGGGGSGGGS-DVVMTQSPSFLSAFVGDT1T1TCRASQG1YNYLAWYQQKPGKAPK LLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVE Vaccines against conformation-dependent or non-peptide antigens, on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor vaccines (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX Disclosure; Page 5-9; 36pp; German. AAB45992 standard; Peptide; 240 AA Human MUC-1 scFv clone Q1.3 99DE-1024405 99DE-1043016 29-MAY-2000; 2000WO-DE01809 (first entry) Karsten U; WPI; 2001-049937/06. WO200073430-A2. 27-MAY-1999; 09-SEP-1999; Homo sapiens 07-DEC-2000 23-MAR-2001 240 IK 241 Goletz S, AAB45992; ÷ 13 19 118 180 238 121 61 AAB45992 ద d g õ ò $^{\circ}$

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Thu Aug

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having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope mimics having one of 16 9-17 residue amino acid sequences, all fully in the specification; (5) antiidiotypic antibody fragments against the TF antigen having one of 24 approximately 200 residue amino acid sequences, fully defined in the specification; (6) TF carbohydrate epitope mimetics having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; and (7) DNA sequences encoding the fragments and derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasites. The vaccines are effective in cases where vaccination has previously not been possible.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -dependent antigen; antibody; cancer;
; virucidal; antibacterial; TF antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccines against conformation-dependent or non-peptide antigens, based
                                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG 120
                                                                                                                                                                                                                                                                                                                                                                              GGGPGGGGGGGGS-DVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPK 179
                                                                                                                                                                                                                                                                                         ssyamswvrqapgkglewvssinyngdatsy 60
                                                                                                                                                                                                                                                                          DDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                       ore 984; DB 22;
ed. No. 6.2e-59;
Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment P3.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUC1; human; vaccine; conformation antiidiotypic antibody; cytostatic antiparasitic; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TF anti-idiotype antibody
                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                       77.0%;
ilarity 78.9%;
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This invention describes a novel vaccine (VI) against

conformation-dependent antigens (CDA) comprising DNA (I) and/or an

antibody, or peptide which immunologically imitates CDA, is new. (I)

encodes a region of an antiddotypic antibody (Ab2) or another peptide

which: (a) specifically binds to the binding site of an antibody (Ab1)

or an antigen binding molecule; and (b) immunologically mimics the

initial antigen. The epitope is partially or completely

conformation-dependent, and has an immunogenic structure defined by a

specific spatial conformation of amino acids. (I) is used in the form

of linear or circular naked DNA and/or whith a viral vector and/or

adjuvants. The products of the invention have cytostatic, virucidal,

antibacterial and antiparasitic. The invention also describes (I) a

corresponding vaccine (V2) against antigens which are not proteins or

peptides, as defined above but which have epitopes which show an

corresponding vaccine (V2) against the MUC1-conformation epitope

antidiotypic antibody fragments against the MUC1-conformation epitope

fully defined in the specification; (4) MUC1-conformation epitope

chaving one of 16 9-17 residue amino acid sequences, all fully in the

specification; (5) antidiotypic antibody fragments against the FF

antigen having one of 24 approximately 50 residue amino acid sequences,

fully defined in the specification; (6) FF carbohydrate epitope mimetics

chaving one of 25 7-13 residue amino acid sequences, all fully defined in

the specification; (5) antidiotypic antibody fragments against the FF

antigen having one of 27 vala residue amino acid sequences, all fully defined in

the specification; and (17) DNA sequences encoding the fragments and

the specification; and (17) NA sequences cocoding the gramming and

chaving one of 27 7-13 residue amino acid sequences, all fully defined in (17) NA sequences and encoding the gramming and encoded the specification and parasites. The vaccines are effective in cases where vaccination has any and parasity.
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peptide which mimics the antigen, useful e.g.
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Pred. No. 1.8e-58;
3; Mismatches 27;
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MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;

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conformation ubscripts a novel vaccine (vi) against conformation-dependent antigens (CDA) comprising DNA (1) and/or an antibody, or peptide which immunologically imitates CDA, is new. (I) encodes a region of an antidiotypic antibody (AD2) or another peptide which immunologically imitates CDA, is new. (I) which: (a) specifically binds to the binding site of an antibody (AD1) or an ontigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form of linear or circular naked DNA and/or with a viral vector and/or action antipacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which show an corresponding vaccine (V2) against which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) human completed in the specification; (4) molf-conformation epitope having one of 31 approximately 60 residue amino acids sequences, all fully in the specification; (5) antidiotypic antibody fragments against the TF antigen having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics thaving one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics thaving one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics antigen having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics antigen having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope and carbor, and infectious diseases, e.g. caused by prices, vaccin
 virucidal; antibacterial; TF antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccines against conformation-dependent or non-peptide antigens, based on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor vaccines
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antildiotypic antibody; cytostatic; antiparasitic; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SSGGGGGGGGGGGGGDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKA 177
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREP-HNTDAFDIWGRGTLVTVSS
                                     158 GGGSGGGGGGGDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQ
                                                            180 LLIYAASTLQSGVPSRFSGSGGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVE
                                                                                                                                                                                                                                                                                                                                                                               1 QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY
        GGGGPGGGGGGGGSDVVWTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPK
                                                                    DDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY
                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDA----FDIWGRGTLVTV
                                                                                                                                                                                                                                                                                                                                                                                                              PK----LLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYP--LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDYSFSISNLEPEDIATYYC---LHYDNEHT
                                                                                                                                                                                                   Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                             cDNAs encoding VH and VL of a 79) cross-reactive with NCA-95 olecule (scFv).";
                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                Kim I.J., Choi I.H., Lee S.D. 19 H.K.;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                          Q921A6;
Q921A6;
Q921A6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mui
                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                         48;
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. No. 5.1e-54;
ismatches 48;
                                                                                                                                                                                                                                                                                                                   6887248E9C771
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                                                                                                                                                                                                                              57.0%; Score ilarity 56.4%; Pred. Conservative 41; Mis
                                                                                                                                                                                                                                                                                                                                                                       1 QVRLQQSGGLVQPGRSLRLSCAASGFTF
       PRT
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26086 MW;
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Best Local Similarity
Matches 141; Conser
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278 IK 279
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SEQUENCE ......
STRAIN=BALB/C;
Cui D., Zeng G., Yan X., Li X., Su C.;
Cui D., Zeng G., Yan X., Li X., Su C.;
Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240168; AAK43733.1; -.
NON TER 218 218
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
"An antibody fragment2A3 specific for native lysozyme:Isolaion from
human synthetic phage display library and characterization.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049915; BAB16829.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                   their precursors improving irradiation in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLVTVSSG
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                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSCMTWNSGSIGY
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                                                                                                                                                                                                                                                                                  Ren D., Zhao T.,
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Catarrhini; Hominidae;
                          Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 APKLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQ
                                                                                                                                                                                                                                                                                  Cui D., Zeng G., Yan X., Wang F., Tian F.,
                                                                                                                                                                                                                                                                                                                            "Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000).
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 Created)
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01-MAR-2001 (TrEMBLrel. 16, Cres
01-MAR-2001 (TrEMBLrel. 16, Last
01-DEC-2001 (TrEMBLrel. 19, Last
SINGLE CHAIN FV (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Cr
NCBI_TaxID-9606;
                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
19,
19,
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                      01-DEC-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. MRP5 (FRAGMENT).
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              PRELIMINARY;
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118 AA;
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Best Local Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                  Matches 111;
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SEQUENCE
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                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                        61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAFDIWGRGTLV 115
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                                                                                                          Length
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                                                                           A45EC3B84788 CRC64
                                                                                                                                                                                                                                                                   09UL71;
09UL71;
01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                         Score 490.5; DB 4;
Pred. No. 2.6e-34;
9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478; DB 4;
No. 3.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                        Kalis N.N.,
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fetus.";

Clin. Immunol. Immunopathol. 87:184-19

EMBL; AF035043; AAD56279.1; -..

HSSP; P01772; 2FB4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

NON_TER 121 121

SEQUENCE 121 AA; 13154 MW; 2F0450
                                                                           24F1
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
"Myosin-reactive autoantibodies in
                                                                112
12243 MW;
                                                                                                         38.4%;
ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.4%;
76.9%;
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IPR003596; Ig_v
           Pfam; PF00047; ig; 1.
SMART; SM00409; iG; 1.
SMART; SM00406; iGv; 1.
SMART; SM00410; iG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                112
112 AA;
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Best Local Simi
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Best Local Simi
Matches 93;
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   InterPro;
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RESULT

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ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTDAF-----DIWGRGTL 114
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                     096BB9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID+9606,
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                            TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D0633949F2AC149D CRC64;
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---YAA-TSQVLLPSK 220
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O9UL91;
01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAY-2001 (TrEMBLrel, 13, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.6%; Score 468; DB 4; L
49.8%; Pred. No. 1.6e-31;
:ive 27; Mismatches 35;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035023; AAD56259.1;
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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RESULT Q9UL71

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104 AA;
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Best Local Similarity
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Matches 85; Conser
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NON_TER
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NON_TER
NON_TER
SEQUENCE
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Q9UL70
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                                                                                        'DDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
                                                                                                                                                             (FRAGMENT).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Primates; Catarrhin1; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                  Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                       09UL79 PRELIMINARY; PRT; 108 AA.
09UL79;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09UL87;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e 452; DB 4; L6
. No. 4.6e-31;
ismatches 13;
                             , 5e-32;
les 12;
                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-192(1998)
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                467.5;
No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.3%; Pred.
Matches 87; Conservative 7; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in fetus.";
              Query Match
Best Local Similarity 78.0%; Pred.
Matches 92; Conservative 13; Mi
                                                                                     13; Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11787 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA;
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NON_TER
SEQUENCE
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09UL79
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135 DVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPCKAPKLLIYAASTLQSGVPS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 CAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGYADSVKGRFTISRDNAKNSLYL
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                          Wu X., Liu B., Van der merme ...... Young D.C.;
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%; Score 451; DB 4; Length 104;
81.7%; Pred. No. 5.3e-31;
tive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                             611D1A3F40E96E7B CRC64;
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 QMNSLRAEDTAVYYCARE-----PHNTDAFDIWGRGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QMNSLRAEDTALYYCAKANYYGSGSYYTEYFQHWGQGTLVTVSS 104
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                                                                                               fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035027; AAD56263.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -.
                                                                                                                                                                                                                                                                                                                                                             11598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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SEQUENCE FROM N.A.
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SMART; SM0040
                                                                                                                                                                                                                                                                                                                                                                                                                      (FRAGMENT).
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NON_TER
SEQUENCE
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09UL93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                            S.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 108;
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                                                                                              REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LISYPLTFGGGTKVEIK 241
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                                                                                                                                                                                                                                                                                            rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64
                                                                                                                                                                                                                                                         Kalis N.N., Berney
                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
O9UL70
O9UL70;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B7BEDC3E41FCCA37
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Pred. No. 8.2e-31;
5; Mismatches 14
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                                                                                                                                                                                                                                                                                                                               -192(1998)
                                                                                                                                                                                                                                                                                                         fetus.";
Clin. Immunol. Immunopathol. 87:184-19
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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EMBL; AF035024; AAD56260.1; -.

HSSP; P01772; 2FB4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.
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12437 MW; ED57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.1%; Score Best Local Similarity 82.2%; Pred. Matches 88; Conservative 5; Mis
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Young D.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         55°.
19; 1.
IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
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                                                                                                             (FRAGMENT)
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
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                                                                                                                                                                                                                                                                                                                        119
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-----LNYWGOGTLVTVSS 113
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                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                     Young D.C.; Myosin-reactive autoantibodies in rheumatic carditis and normal
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  Length 113;
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                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 RFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090L77;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL93;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
(FRAGMENT).
Query Match 34.9%; Score 446; DB 4; I Best Local Similarity 71.4%; Pred. No. 1.6e-30; Matches 85; Conservative 15; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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Pred. No. 4.7e-30;
5; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; 1REI.
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.o; IPRUC.
ro; IPRO03596,
PF00047; ig; 1.
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llarity 81.3%;
Conservative 5
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InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
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TISSUE-MAMMARY GLAND:

I Sogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

I I Sogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Nagatsuma M., Hosoiri T., Kaku Y., Ishii S., Kawai Y., Takiguchi S.,

Natanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Natanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Namamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AK027379; BAB55072.1; -.

SEQUENCE 494 AA; 53088 MW; 9AID7AEB5AEE4C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:||||
DTAMYYCA--GGGGLGLGYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                DTAVYYCAREPHNTDAFDIWGRGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                    5;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ14473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO
SAPIENS SNC73 PROTEIN (SNC73) MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

34.4%; Score 439.5; DB 4; Length 494;

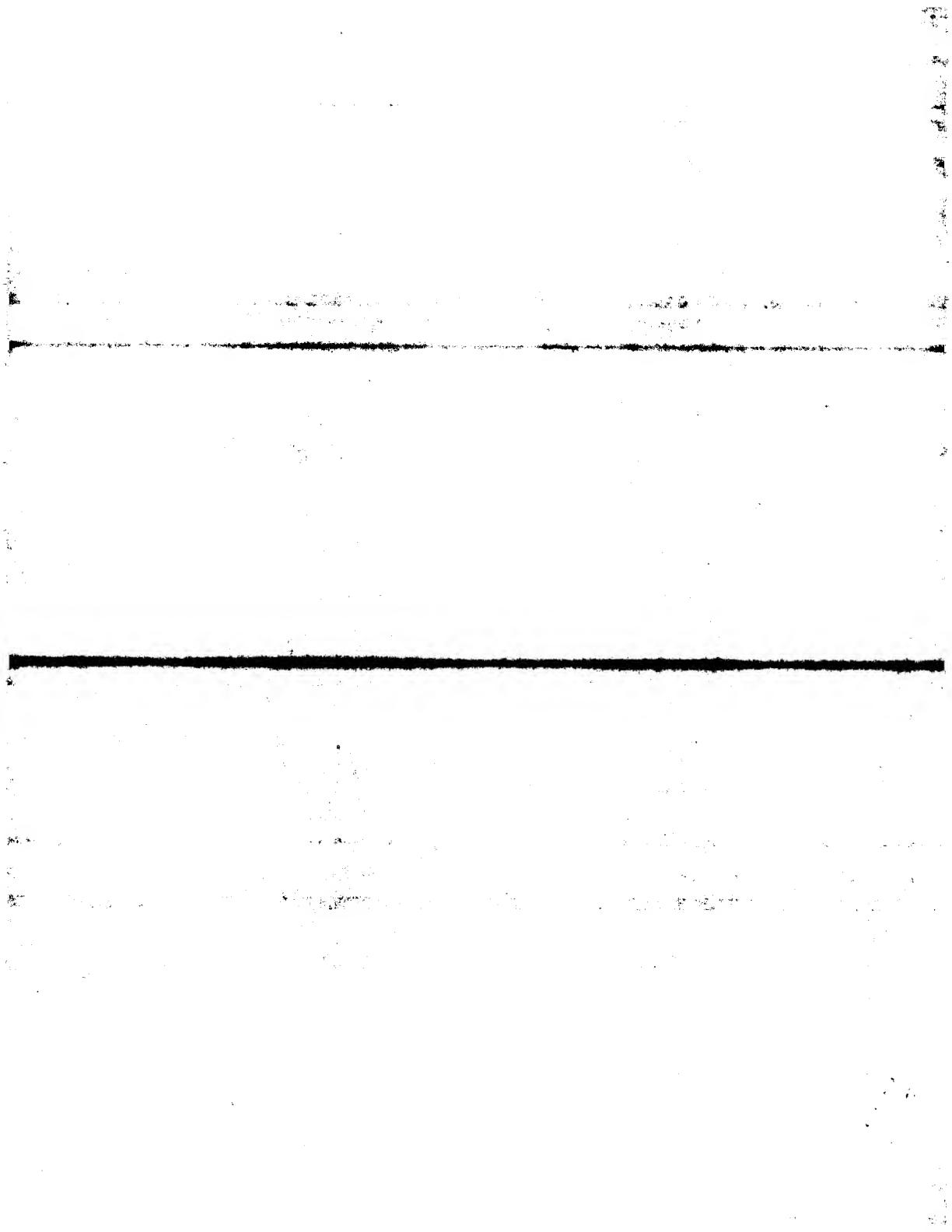
Best Local Similarity 72.1%; Pred. No. 3.3e-29;

Matches 88; Conservative 11; Mismatches 20; Indels 3
                                                     Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                  Length 116,
                                                                                                                                                                                                                                                                                                                e 440; DB 4; Length 1]
. No. 5.2e-30;
ismatches 17; Indels
                                                                                                                                                                                                                                                                   0DA0348154DD6061 CRC64;
                                                                                                                    84-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 AA
                                                                             "Myosin-reactive autoantibodies in i
fetus.";
Clin. Immunol, Immunopathol, 87:184-
EMBL; AF035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 116 116
SEQUENCE 116 AA; 12434 MW; 0DA03
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L..
Young D.C.;
                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 72.9%; Pred
Matches 86; Conservative 13; M
                                                                                                                                                                                                                                                                                                                                                                                61 DSVKGRFTISRDNSKNTLYLQMNSLRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DSVKGRFTISRDNAKNSLYLOMNSLRAE
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11
Db 140 SS 141
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Search completed: August 15, 2002, 16:35:38 Job time: 798 sec



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Compugen Ltd
  GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

August 15, 2002, 16:36:09; Search time 28.14 Seconds (without alignments) 331.607 Million cell updates/sec Run on:

US-08-779-457-50 1278 Title: Perfect score:

......CQQLISYPLTFGGGTKVEIK BLOSUM62 Gapop 10.0 , Gapext 0.5 1 QVRLQQSGGLVQPGRSLRL. Scoring table: Sequence:

241

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

es Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summari

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ARIES SUMM

	Description		P01771 homo sapien	P01768 homo sapien	PO4430 homo sapien	P01782 homo sapien	P01770 homo sapien	9 hamo		P01610 homo sapien	homod	O homo	1 homo	2 homo	9 homo	homo	1 homo	homod	9 пото	mus m	P01772 homo sapien	. P01597 homo sapien	homo	homo	homod	9 homo	mus m	homo	homo	homo	5 homo	homo	3 homo	P01601 homo sapien
SUMMARIES	ID		HV3J_HUMAN	HV3G_HUMAN	KV1V_HUMAN	HV3U_HUMAN	HV3I_HUMAN	KV1G_HUMAN	KV1S_HUMAN	KV1R_HUMAN	KV1W_HUMAN	KV1H_HUMAN	HV3T_HUMAN	KV1Y_HUMAN	HV3H_HUMAN	KV1X_HUMAN	KV1L_HUMAN	KV1F_HUMAN	KV1P_HUMAN	KV5D_MOUSE	HV3K_HUMAN	KV1E_HUMAN	KV1K_HUMAN	HV3C_HUMAN	KV1B_HUMAN	KV1Q_HUMAN	HV16_MOUSE	KV1M_HUMAN	KV10_HUMAN	KV1D_HUMAN	KV1N_HUMAN	HV3D_HUMAN	HV3B_HUMAN	KV1I_HUMAN
	n DB		1 1																														٦ ۲	_
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æ	Query Match Length		35.6	35.6	34.9	34.5	34.4		34.2	4		m.	ω.	ω.	ر	ω.	32.9	ä	ci.	32.6	ä	4	તં	ä	•		•		ď	2	32.0	ď	Ξ.	31.7
	Score)	455	454.5	446	441.5	439	438	437	434	433	-	427.5	426	424.5	422	420	419	418	416	415.5	413	413	412	411	411	410.5	410	410	409.5	409	409	406.5	405
	Result No.) : ·	П	7	ო	4	Ŋ	9	7	σ	თ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32

	P01602 homo sapien										
KV1C_HUMAN	KV1J_HUMAN	KV1T_HUMAN	HV3F_HUMAN	HV3L_HUMAN	HV38_MOUSE	HV32_MOUSE	HV40_MOUSE	KV1A_HUMAN	HV3E_HUMAN	HV01_CANFA	HV34_MOUSE
-	_	⊣	Н	_	-	Ļ	Н	-	-	Н	7
108	117	109	115	119	119	115	119	108	120	114	113
31.6	31.5	31.4	31.1	30.9	30.8	30.8	30.7	30.7	30.7	30.6	30.4
	0.5	01.5	398	395	393.5	393	392.5	392	392	391.5	389
404	4	7									

ALIGNMENTS

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Gaps
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                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region HIL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           1 QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=79124695; Pubmed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:553-560(1979). .
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                  Length 121;
                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                  Ouery Match 35.6%; Score 455; DB 1; Length 1:
Best Local Similarity 71.1%; Pred. No. 6.7e-30;
Matches 86; Conservative 13; Mismatches 20; Indels
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(Rel. 01, Last sequence update)
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                   STANDARD;
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21-JUL-1986 (
                  HV3J_HUMAN
P01771;
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MEDLINE-81013859; PubMed-6774332;

Lehman D.W., Putnam F.W.;

Lehman D.W., Putnam F.W.;

Lehman D.W., Putnam F.W.;

Location of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

PATIENT WITH MACROGLOBULINEMIA.

PATIENT WITH MACROGLOBULINEMIA.

PATIENT WAS ISOLATED FROM THE PLASMA OF A HSSP; PO1772; 21G2.

RICHARD: PRO03596; Ig_W.

RICHARD: PRO03596; Ig_W.

RICHARD: PRO03596; Ig_W.

RICHARD: SMART; SMO0406; IGV; 1.

Immunoglobulin V region.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                  Vertebrata; Euteleostomi;
i; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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ed. No. 7.4e-30;
Mismatches 15;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region BAN.
Homo sapiens (Human).
          ion update)
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15-JUL-1999 (Rel. 38, Last annotation upda Ig heavy chain V-III region CAM. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vemammalia; Eutheria; Primates; Catarrhini;
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MEDLINE-86174817; PubMed-3083240;

Dwulet F.E., O'Connor T.P., Benson M.

"Polymorphism in a kappa I primary (Polymorphism in a kappa I primary (Polymorphism in a kappa I primary (Poly I mmunol. 23:73-78(1986).

FIR; A01878; K1HUBN.

HSSP; P80362; IWTL.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003066; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 18:4054-4067(1979).
-1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION 1
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
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Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
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  FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                     Score 446; DB 1;
Pred. No. 3.1e-29;
9; Mismatches 14;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region DOB.
Homo sapiens (Human).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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MEDLINE-77070267; PubMed-1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal IgGl immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
HOPPE-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Catarrhini; Hominidae; Homo.
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1.2e-28;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region GAL.
Homo sapiens (Human).
                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region NIE.
Homo sapiens (Human).
                                                            119 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Ponstingl H., Hilschmann N.; The rule of antibody structure.
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-77070269; PubMed-826475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF000047; ig; 1,
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13242 MW;
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                                                            STANDARD;
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119
119 AA;
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les 85; Conser
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                                                      HV31_HUMAN
P01770;
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P01599;
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Best Local S
Matches 85
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SEQUENCE
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RESULT 5
HV3I_HUMAN
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Laure C.J., Watanabe S., Hilschmann N.;

"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), I. The amino acid sequence of the L-chain of tappa-type, subgroup I.";

Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

MACROGLOBULIN.

PIR; A01867; K1HUGL.

RISSP; P01607; 1REI.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

R SMART; SM00406; IGV; 1.

Immunoglobulin V region.
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Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

L Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

C -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

R PIR, A01877; K1HUWS.

R HSSP; P80362; 1WTL.

R HSSP; P80362; 1WTL.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR00406; IGV.

R INTERPRO; IPR00406; IRR00406; IGV.

R InterPro; IPR00406; IRR0040
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Wes. ,
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAMEWORK-2.
COMPLEMENTARITY - DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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Pred. No. 1.3e-28;
4; Mismatches 16
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llarity 81.3%;
Conservative
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Best Local Simmatches 87;
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P01611;
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Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
PIR; A01876; K1HUWE.
                                                                                                                                    DVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 194
                                                                                                                                             SHWLAWYQQKSGKAPKLLIYSASSLENGVPS 60
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG kappa chain V-I region WEA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                            Length 108;
      EMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
                    EMENTARITY - DETERMINING - 3
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EMENTARITY-DETERMINING-3
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                                                                B14A649A60E45 CRC64
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                                                                                            re 437; DB 1; L4
1. No. 1.6e-28;
fismatches 12;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoqlobulin V region; Mor
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illarity 78.5%;
Conservative
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llarity 78.5%;
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P01610;
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Matches 84
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KV1R_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GGGSDVVMTOSPSFLSAFVGDTITITCRASQGIYNYLAWYQQKPGKAPKLLIYAASTLQS 190
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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Pred. No. 4.1e-28;
; Mismatches 18; Indels
                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Walker precursor.
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Last sequence update)
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HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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MEDLINE=85014148; PubMed*6091049;
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P01600;
21-JUL-1986
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P04431;
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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ISOLATED FROM A WALDENSTROM'S
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Ig kappa chain V-I region Hau.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                    Watanabe S., Hilschmann N.;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I
"The primary structure of a monoclonal kappa-type immunoglobulin I
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No. 5.8e-28;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region GAL.
Homo sapiens (Human).
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COMPLEMENTAR
FRAMEWORK-3.
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HOPPE-5c,
HOPPE-5c,
HISCELLANEOUS: 161,
PIR; A01868; K1HUHU.
HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
R Pfam; PF00047; 1g; 1.
NR MART; SM00406; IGV; 1.
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P01781;
21-JUL-1986 (Rel.
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MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
"Comparison of altered domain interactions in immunoglobulin
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region WAT.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=81267384; PubMed=6167731;

Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,

Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,

Popp R.A., Solomon A.;

"Characterization and preliminary crystallographic data on the VI
related fragment of the human kI Bence Jones protein Wat.";

J. Mol. Biol. 147:185-193(1981).

J. Mol. Biol. 147:185-193(1981).

PDB; 1WTL; 01-NOV-94.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R SMART; SM00406; IGV; 1.

SMART; SM00406; IGV; 1.

Eminuoglobulin V region; Bence-Jones protein; 3D-structure.
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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larity 69.7%; Pred. No. 9.9e-28;
Conservative 11; Mismatches 22;
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Biochemistry 33:14848-14857(1994)
MACROGLOBULIN.
PIR; A02064; M3HUGL.
HSSP; P01772; 2IG2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
NON_TER 116 116
SEQUENCE 116 AA; 12730 MW;
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ırrhini; Hominidae; Homo.
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                                                                                                                                                       195 RESGSGSGTEFTLTISSLOPEDFGTYYCQQLISYPLTFGGGTKVEIK 241
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                 DB 1;
1.2e-27;
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                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region GA.
Homo sapiens (Human).
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Daudi precursor.
Homo sapiens (Human).
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                                     . No. 1.2e
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Ismatches
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Mammalia; Eutheria; Primates; Catarrhin;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-74175307; PubMed-4208843; Florent G., Lehman D., Putnam F.W.; Three switch point in mu heavy chains Biochemistry 13:2482-2498(1974).

-1- MISCELLANEOUS: THIS CHAIN WAS IS( MACROGLOBULIN. PIR; A02052; M3HUGA. HSSP; P01772; 21G2. InterPro; IPR003006; 1g_MHC. InterPro; IPR003596; 1g_V. Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1.
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122
13166 MW;
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Best Local Similarity 64.8%;
Matches 79; Conservative 19
                                                   Conservative
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122 AA;
                             Best Local Similarity
Matches 80; Conser
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P01769;
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P04432;
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NON_TER
SEQUENCE
                   Ouery Match
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KV1X_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type."; Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
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                                                                                                            Klobeck H.G., Combriato G., Zachau H.G.; "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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   Primates; Catarrhini; Hominidae; Homo
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Mismatches
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                                                                   SEQUENCE FROM N.A.
MEDLINE-85014148; PubMed-6091049;
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or send a...
FMBL; X00966; CAA25...
PIR; A01884; K1HUDI...
HSSP; P80362; 1WTL...
InterPro; IPR003006; Ig_MHC...
R InterPro; IPR003596; Ig_V...
JR Pfam; PF00047; ig; 1...
DR SMART; SM0406; IGV; 1...
Immunoglobulin V region; SigratGNAL...
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7 23 129
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75.7%;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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-:- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

R PIR; A01870; KIHUKU.

R HSSP; P01607; IREI.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_v.

R Ffam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Bence-Jones protein.

FRAMEWORK-1.

DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

T DOMAIN 35 49 FRAMEWORK-2.

DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

T DOMAIN 57 88 FRAMEWORK-3.

DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

T DOMAIN 99 107 FRAMEWORK-4.

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Pred. No. 3.6e-27;
9; Mismatches 17; Indels
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Best Local Similarity 75.7%;
Matches 81; Conservative
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:10 Search completed: August 15, 2002, 16:36 Job time: 720 sec

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Compugen Ltd
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

earch time 54.95 Seconds (without alignments) 421.429 Million cell updates/sec Search time August 15, 2002, 16:25:02; Run on:

score: Title: Perfect

... COQLISYPLTFGGGTKVEIK US-08-779-457-50 1278 1 OVRLQQSGGCLVQPGRSLRL. Sednence:

241

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

SUMMARIES

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ALIGNMENTS

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States to 6-Jan-1995 #text_change 06-Jan-1995  
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995  
C; Accession: S41374
C; Accession: Acce
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ŭ, Length 249; Indels DB 2; :99 .4e-44 Query Match
Best Local Similarity 53.7%; Pred. No. 3.46
Matches 132; Conservative 43; Mismatches

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Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functic A;Reference number: A56446; MUID:95229583 from

operate

#text_change 23-Jul-1999

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31595
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human 1mmunoglobulin diversity operat
A; Reference number: S31585
A; Reference number: S31585
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-128 <CUI>A; Molecule type: mRNA
Cross-references: EMBL: Z14171; NID: g31007; PIDN: CAA78540.1; PID: g31008
C; Superfamily: immunoglobulin
C; Superfamily: immunoglobulin
F; 23-106/Domain: immunoglobulin homology <IMM>
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Matches 104; Conservative
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   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53 specific single-chain antibody Pab421
C; Species: Homo sapiens (man)
C; Date: 15-May-1997 #sequence_revision 15·
C; Accession: JC5322
R; Jannot, C.B.; Hynes, N.E.
Blochem. Biophys. Res. Commun. 230, 242-2/
A; Title: Characterization of scFv-421, a /
A; Reference number: JC5322; MUID:97168950
A; Accession: JC5322
A; Molecule type: mRNA
A; Residues: 1-233 <JAN>
A; Experimental source: hydricloma cell
C; Comment: This protein specifically bind
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Pred.
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                                                                                                            54.5%; Score
llarity 54.8%; Pred
Conservative 41; M
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50.8%;
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Best Local S
Matches 122
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C; Species: mann.
C; Species: mann.
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Accession: S31118
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuu: Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third command: S31118
A; Reference number: S31104; MUID:92111633
A; Reference number: S31104; MUID:92111633
A; Accession: S31118
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-121 < RAA>
A; Cross-references: EMBL: X62969
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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Pred. No. 1.8e-33;
0; Mismatches 5;
                                                 3,
   DB 2;
 Score 562.5; DB 2 Pred. No. 3.4e-34;
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                                               11; Mismatches
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86.0%;
Similarity 87.5%;
5; Conservative 11
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C;Species: Homo sapiens (man)
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chain V region - human (fragment)
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C; Date: 21-Dec-1990 #sequence_revision
C; Accession: F36005
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llarity 86.7%;
Conservative
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                                                                          and short diverse third compler
                                         M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_cnange zs-Julitzers C; Accession: S31104
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M. Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse the A; Reference number: S31104
A;Reference number: S31104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-121 <RAA>
A;Residues: 1-121 <RAA>
A;Coss-references: EmBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
A;Coss-references: EmBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                              translation not shown
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        6-May-1995 #text_change 23-Jul-1999
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8.4e-33;
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Mismatches 7;
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Ig heavy chain V region (clone alpha-THY-32)
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R; Mariette, X.
Submitted to the EMBL Data Library, October A; Reference number: $30520
A; Reference number: $30520
A; Accession: $30532
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-123 < MAR>
A; Residues: 1-123 < MAR>
C; Superfamily: immunoglobulin V region; imm C; Keywords: heterotetramer; immunoglobulin F; 15-98/Domain: immunoglobulin homology <IM
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C;Date: 06-Jan-1995 #sequence_revision 0
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85.1%; Pred.
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S30532
Ig heavy chain V region - human
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Best Local Similarity
Matches 103; Conser
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Matches 101; Conser
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                                         #text_change 23-Jul-1999
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C; Species: Homo sapiens (man)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-(C; Accession: S36273
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, EMBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage A; Title: Human anti-self antibodies with high specificity from phage A; Reference number: S36256; MUID: 93178448
A; Accession: S36273
A; Accession: S36273
A; Accession: S36273
A; Catus: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA
A; Residues: 1-120 <GRI>A; Cross-references: EMBL: Z18834; NID: 933116; PIDN: CAA79286.1; PID: 9; C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                               J.M.; Embleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-,
C; Accession: 511239
R; Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A; Title: Acids Res. 18, 4927, 1990
A; Title: Nucleotide sequences of the cDNAs encoding the V-regions of A; Reference number: 511239; MUID:90370490
A; Reference number: 511239; MUID:90370490
A; Accession: 511239
A; Accession: 511239
A; Catus: preliminary
A; Molecule type: mRNA
A; Residues: 1-145 < FEL>
A; Cross-references: EMBL:X53613; NID:923865; PIDN:CAA37675.1; PID:9
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < IMM>
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Pred. No. 1.2e-31;
5; Mismatches 9;
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Pred. No. 6e-31;
2; Mismatches
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Gypecies: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse thin A; Reference number: S31104; MUID:92111633
A; Reference number: S31107
A; Reference not shown; translation not shown A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-119 <RAA>
A; Reference number: PC4279; MUID:97236289
A; Accession: PC4281
A; Molecule type: protein
A; Residues: 1-123 <SUZ>
C; Comment: This antibody is commonly found in systemic autoimmune diseases
C; Superfamily: immunoglobulin V region; immunoglobulin homology
E; 15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                     QVRLQQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY
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llarity 74.6%; Pred. No. 9.7e-29;
Conservative 15; Mismatches 12;
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Pred. No. 1e-28;
7; Mismatches 1:
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ilarity 82.9%;
Conservative
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Matches 92; Conser
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Best Local Similarity
Matches 91; Conserv
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C; Accession: PC4281
R; Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Blochem. Biophys. Res. Commun. 232, 101-106, 1997
A; Title: Molecular.cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
                                                gene
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    R;Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571

A;Accession: F36005
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R; Tomlinson, 1.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fi
A; Reference number: $26885; MUID: 93021117
A; Reference number: $26885; MUID: 93021117
A; Reference number: $26885; MUID: 93021117
A; Reference number: $26927
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-98 < TOM>A; Residues: 1-98 < TOM>A; Residues: Immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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ismatches 1;
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No. 1.5e-29;
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C; Genetics:
A; Gene: GDB:IGH@; IGHDY1
A; Cross-references: GDB:118731; OMIM:14691(
A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin V region; imm
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IN
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Best Local Similarity
Matches 90; Conserv
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A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
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Scoring table:
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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    /cgn2_6/ptodata/2/paa/US080_COMB.pep: *
    /cgn2_6/ptodata/2/paa/US080_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	Length [ID	Description
ىر	1278		- 1	11	US-08-779-457-50	Sequence 50, Ap
2	1086.5	85.0		-	PCT-US01-19110-1310	Sequence 1310, F
ω	1086.5	85.0	251	22	US-09-880-748-1310	Sequence 1310,
4	1070.5	83.8	251	H	PCT-US01-19110-922	Sequence 922, Ap
رن ن	1070.5	83.8	251	22	2 US-09-880-748-922	Sequence 922, I
σ	1065.5	83.4	251	ш	PCT-US01-19110-1320	Sequence 1320, 1
7	1065.5	83.4		22	US-09-880-748-1320	Sequence 1320, Ap

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US-09-250-056B-2 US-09-880-748-82 US-09-880-748-82 PCT-US01-19110-261 US-09-880-748-261 PCT-US01-19110-164 US-09-880-748-280 US-09-880-748-1945 PCT-US01-19110-1945 US-09-880-748-1177 US-09-880-748-1177 US-09-880-748-1177 PCT-US01-19110-2043 US-09-880-748-2019 PCT-US01-19110-2043 US-09-880-748-2019 PCT-US01-19110-2043 US-09-880-748-2019 PCT-US01-19110-2003 PCT-US01-19110-2003 PCT-US01-19110-2003 PCT-US01-19110-2003 PCT-US01-19110-2005 PCT-US01-19110-2005 PCT-US01-19110-1922 US-09-880-748-1922 US-09-880-748-1922 PCT-US01-19110-1922 PCT-US01-19110-1922 PCT-US01-19110-1922 PCT-US01-19110-1922 PCT-US01-19110-1921 PCT-US01-19110-1921 PCT-US01-19110-1921 PCT-US01-19110-1921	PCT-US01-19110-936 US-09-880-748-936 US-09-250-056-2
82, 261, 261, 280, 280, 194, 194, 193, 1177, 117	Sequence 936, App Sequence 936, App Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-779-457-50
US-08-779-457-
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84.0%;

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REFERENCE/DOCKET NUMBER: P098:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-50
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PCT-US01-19110-1310
; Sequence 1310, Application PC/TUS0119110
; GENERAL INFORMATION:
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                                            PCT-US01-19110-1310
                                                                                                         CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
Query Match
                                                                                   SEQ ID NO 1310
LENGTH: 251
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                                                                                                                                                                                                                                                                                                           APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523PCT
                                                       ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 01/08/9
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Pred. No. 4.9
0; Mismatches
Score
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US-09-880-748-1310
; Sequence 1310, Application US/09880748
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin
SEQ ID NO 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Query Match 85.0%;
Best Local Similarity 84.0%;
Matches 210; Conservative 1
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: Pate
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TITLE OF INVENTION: Antibodies that
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                       ADSVKGRFTISRDNAKNSLYLQMNSLRAEDT
                               GTLVTVSSGGGGPGGGGSGGGSDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQ 171
                                                                                                                                                                                                                     OKPGKAPKLLIYAASTLOSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLT 240
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  FGGGTKVEIK
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); Mismatches 21;
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                              TEFTLTISSLQPEDFGTYYCQQLISYPLT 231
TEFTLTISSLQPEDFGTYYCQQLISYPLT 240
                                                                                             SFLSAFVGDTITITCRASQGTYNYLAWYQ 180
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Sequence 922, Application US/09880748; GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bin FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bin
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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US-09-880-748-922
Sequence 922, Application US/09880748
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PCT-US01-19110-922
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Best Local Similarity
Watches 201; Conserv
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LENGTH: 251
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
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80.4%;
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Pred. No. 4.5e-
l; Mismatches
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; ORGANISM: Homo sapiens US-09-880-748-922
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                                                                                                                                                y TYPE: PRT
; ORGANISM: Homo:
PCT-US01-19110-1320
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US01/19110

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 201; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1320, Appli GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 922
LENGTH: 251
                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 1320
LENGTH: 251
                                                                 Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
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GTLYTVSSGGGGGGGGGGGGGGGDVVMTQSPSFLSAFVGDTITITCRASQGIYNYLAWYQ 171
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                                                                 200;
                                                               Similarity 80.0
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Pred.
                                                                              Score 1065.5; DB 1; Pred. No. 1.2e-83;
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                                                                Indels
                                                                                              Length 251;
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1320
LENGTH: 251
TYDE: DET
RESULT 8
PCT:US01-19110-936; Sequence 936, Ap.
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; ORGANISM: Homo sapiens
US-09-880-748-1320
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US-09-880-748-1320
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Best Local Similarity 80.0%;
Matches 200; Conservative 2:
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  Application
   PC/TUS0119110
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Pred. No. 1.2e-83;
L; Mismatches 20; ]
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
FILE OF INVENTION: Antibodies that Immu-
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/191
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
                                             FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,74

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER: 05/293,499

PRIOR FILING DATE: 2001-05-25
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US-09-880-748-936
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NUMBER
SOFTWARE: FR
TO ID NO 936
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Best Local Similarity 81.0%;
Matches 204; Conservative 1:
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SEQ ID NO 936
LENGTH: 253
                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruben et al
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                                         PatentIn
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Pred.
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xt Immunospecifically Bind BLyS
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RESULT 10
US-09-250-056-2
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; ORGANISM: Homo
US-09-880-748-936
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Best Local S
Matches 204
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LOCATION: (184)..(190)
OTHER INFORMATION: VL-CI
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marks, James D
APPLICANT: Poul, Marie A
TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Al
CURRENT APPLICATION NUMBER: US/09/250,056A
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 4
                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                   LENGTH: 242
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                          NAME/KEY: DOMAIN
LOCATION: (50)..(66)
OTHER INFORMATION: VH-CDR2
                                                                                                                                                                                                     NAME/KEY: DOMAIN
LOCATION: (31). (35)
OTHER INFORMATION: VH-CDR1
                                                               NAME/KEY: DOMAIN
LOCATION: (157)..(167)
OTHER INFORMATION: VL-CDR1
                                                                                                            NAME/KEY: DOMAIN
LOCATION: (99)..(108)
OTHER INFORMATION: VH
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ENGTH: 242
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Pred. No. 1.2e-81;
2; Mismatches 25;
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GENERAL INCLUSIONS: GENERAL INTERNALIZING ERB2 AN APPLICANT: Poul, Marie A TITLE OF INVENTION: INTERNALIZING ERB2 AN FILE REFERENCE: 2500.116US3 Internalizing CURRENT APPLICATION NUMBER: US/09/250,056E; CURRENT FILING DATE: 1999-02-12; PRIOR APPLICATION NUMBER: 60/082,953; PRIOR FILING DATE: 1998-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (223)..(;; OTHER INFORMATION: US-09-250-056-2
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US-09-250-056B-2
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                                                                                                                                         OTHER INFORMATION: Description of OTHER INFORMATION: acid sequence NAME/KEY: DOMAIN
LOCATION: (31)..(35)
OTHER INFORMATION: VH-CDR1
NAME/KEY: DOMAIN
LOCATION: (50)..(66)
OTHER INFORMATION: VH-CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 242
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                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM:
                                                                    NAME/KEY: DOMAIN
LOCATION: (157)...(167)
OTHER INFORMATION: VL-CDR1
                                  NAME/KEY: DOMAIN
LOCATION: (184)..(190)
OTHER INFORMATION: VL-
                                                                                                         NAME/KEY: DOMAIN
LOCATION: (99)..(108)
OTHER INFORMATION: VH-CDR3
 OTHER
            NAME/KEY: DOMAIN LOCATION: (223)...
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INFORMATION: VL-CDR3
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N: VL-CDR3
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                                    VL-CDR2
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83.0%;
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1.9e-81;
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CURRENT APPLICATION NUMBER: PCT/USO1/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 244
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Sequence 82, Application PC/TUS0119110

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
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Best Local
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ORGANISM: Homo s
T-US01-19110-82
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                                               KLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFGTYYCQQLISYPLTFGGGTKV
                                   KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKV
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15; Mismatches
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Pred. No. 1.9e
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1.9e-81;
ches 27;
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PCT-US01-19110-261
; Sequence 261, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Imm
; FILE REFERENCE: PF523PCT
; FILE REFERENCE: PF523PCT
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US-09-880-748-82
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CURRENT APPLICATION NUMBER: PCT/US01/191
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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SOFTWARE: Pater
SEQ ID NO 82
LENGTH: 244
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Best Local Similarity 81.3
Matches 197; Conservative
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499

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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 261
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-19110-261
                                                                                                                                                                                                                                                                               FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0
                                                                                                     ; TYPE: PRT
; ORGANISM: HOMO
US-09-880-748-261
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LENGTH: 244
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243
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Search completed: August 15, 2002, 16:34:06 Job time: 766 sec

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RESULT
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ID AAW6
XX AAW6
XX AAW6
XX AAW6
XX AAW6
XX Ob-1
KW Ob-1
KW Ob-1
KW ANO1
XX HOMC
XX AO91
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Best Local s
Matches 1110
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screening a
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Local Similarity 90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obesity protein receptor(s) and related DNA disorders, e.g. obesity, diabetes and high clipid levels
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N-PSDB; AAT98530.
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AAW24052 standard; Protein; 968 æ.

17-MAR-1998 WSX receptor variant (first entry) 6.4.

Human

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DT 17-W
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DE Huma
XX
CA Huma
KW Huma
KW 1195
KW difj
KW Type
KW Carc
KW hype
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OS Home ligand; activator; variant 6.4; iden ligand; activator; antibody; agonist; differentiation; anaemia; treatment; no Type II diabetes; polycystic ovarian dicardiovascular disease; osteoarthritis; hypertension; insulin resistance; hyperhypertriglyceridaemia; cancer; cholalit sapiens entification; purification;
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neoplasia; arteriosclerosis;
disease; is; dermatological disorder;
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                                                                                                                                                                                                                                                    Query Match 77.2%;
Best Local Similarity 100.0%;
Matches 891; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSX receptor and related antibodies and products for diagnosis and therapy, e.g. haematopoiesis or for treating tumours
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l; obesity; diabetes; high cholesterol level;
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rnis sequence :

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English.

the obesity

(OB) receptor B protein. This ogical properties of naturally B receptor proteins and OB and for the treatment of obesity, and high cholesterol levels. The in individual for weight loss or

cosmetic purposes

This sequence represents sequence has one or more occurring OB receptor pro

sequence has one or more of the biolog occurring OB receptor protein. The OB receptor/OB protein complexes are used diabetes, high blood lipid levels and proteins may also be used to treat an weight maintenance required for purely

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Sequence

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      Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for detecting a defective obese protein or leptin receptor (OB-R) in cells. Them method comprises contacting RNA extracted from a cell population (preferably an ovary, prostate, testis, sperm, ova, ovarian follicular or blood cell population) with an coligonucleotide derived from a portion of the human OB-R variant form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are associated with infertility, as they are unable to correctly transduce signals from leptin binding. The detection method can be used to diagnose infertility, or predisposition to infertility, while treatments that inhibit or down regulate the variants, gene therapy to replace them in homozygotes or direct activation of downstream signal transduction can be used to improve fertility.

CC Also described is the use of labelled DNA probes based on the OB-R sequence to screen for other variants.
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N-PSDB;
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Form 1; infertility.
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cytoplasmic domain at the C-terminal end. A claimed method for Cytoplasmic domain at the C-terminal end. A claimed method for Cthis for hybridisation to an oligonucleotide (I) derived from the CC CB-R variant gene, especially from the region beyond nucleotide 2770. Also claimed are methods of: (1) treating obesity by CC administration of an agent that inhibits expression of the OB-R cariant gene; and (2) identification of a compound that can CC supplement activity of leptin by: (1) incubating cells expressing CC OB-R variant first with leptin and then with a test compound, and CC (ii) comparing activation signals between cells treated and not treated with the test compound. Inhibition/down-regulation of the variant OB-R (found in obese people) improves response of cells to CC weight regulation by leptin. Replacing variant OB-R by gene therapy CC (in homozygous individuals) can be used to treat obesity. Labelled probes based on the gene can be used to isolate other variant forms of the receptor gene or to detect the variant gene (e.g. for C determining predisposition to obesity), while the OB-R gene can be used to express variant obsective. While the OB-R gene can be used to express of appetite and hypermetabolic activity). Cells cantibodies that competitively inhibit, neutralise or enhance activity of the variant receptor.
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N-PSDB;
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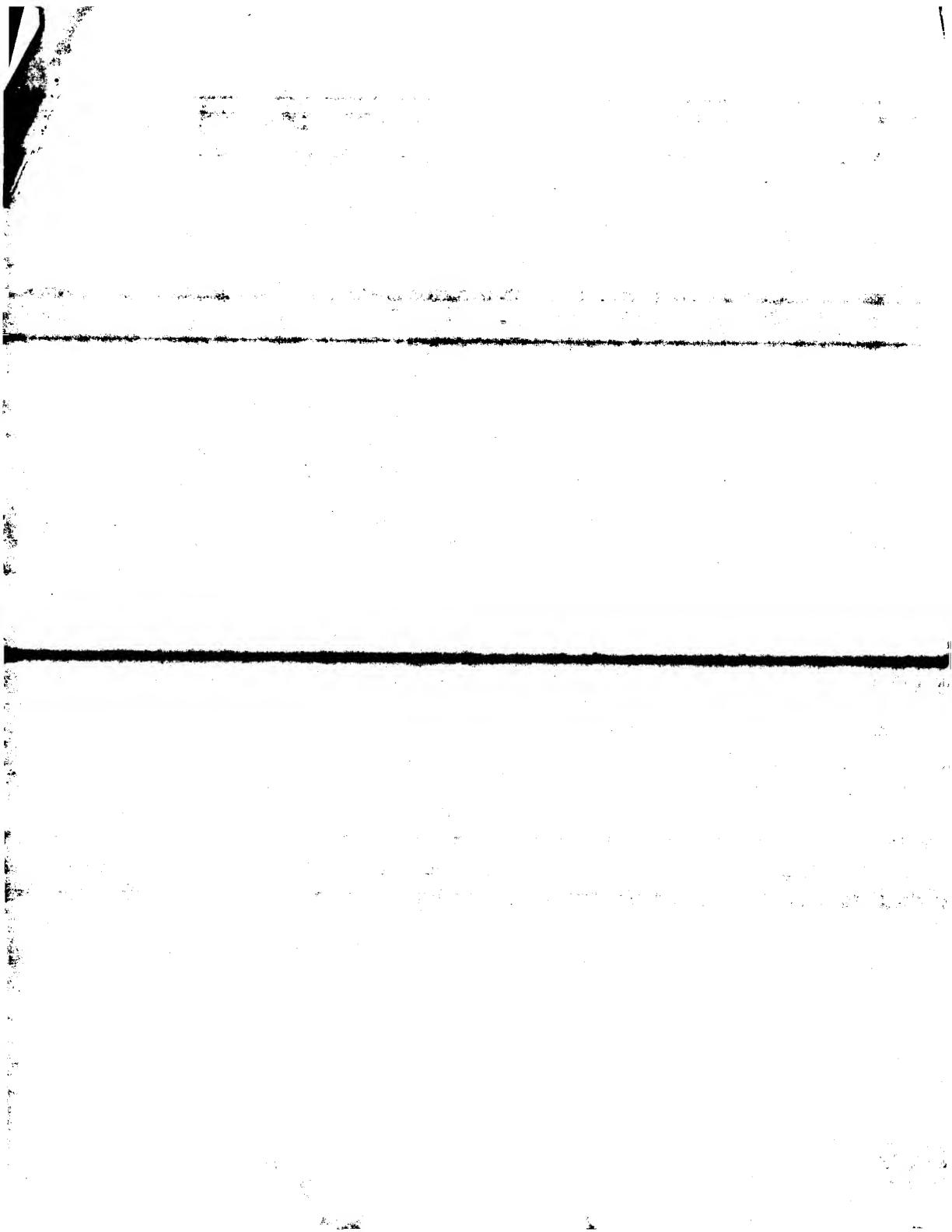
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splicing of a common precursor mRNA. A claimed method for this for hybridisation to an oligonuclectide (I) derived from the CC OB-R variant gene, especially from the region beyond nucleotide (CC 2770. Also claimed are methods of: (1) treating obesity by CC administration of an agent that inhibits expression of the OB-R cc variant gene; and (2) identification of a compound that can cc supplement activity of leptin by: (i) incubating cells expressing cc OB-R variant first with leptin and then with a test compound, and cc treated with the test compound. Inhibition/down-regulation of the cariant OB-R (found in obese people) improves response of cells to comparing activations signals between cells treated and not created with the test compound. Inhibition/down-regulation of the compound in obese people) improves response of cells to compound that can be used to treated on the gene can be used to treat obesity. Labelled created to express recombinant obesity, while the OB-R gene therapy conducted to express recombinant obesity, while the OB-R gene can be used to isolate other variant forms conducted to express recombinant ober (optionally as fusion protein) and cc in standard hybridisation assays. The OB-R gene can also be used to express variant competition of functional OB-R (causing loss of appetite and hypermetabolic activity). Cells creen for (ant)agonists of leptin/OB-R interaction, also to generate antibodies that competitively inhibit, neutralise or enhance activity.
treatment and screen
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                                                                    GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
                                                                                                                GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
                                                                                                                                                                           SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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Mismatches
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COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDM COMPAtible
COMPUTER: IDM COMPATIBLE
COMPUTER: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/53,524
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/56,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/56,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/56,622
FILING DATE: 07-NOV-1995
APPLICATION NUMBER: US 08/56,622
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: US 08/56,622
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 07334/08200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELES: 200154
INFORMATION FOR SEO ID NO: 4:
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GENERAL INFORMATION:
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APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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CITY: Boston
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Best Local Similarity 100.0%;
Matches 1165; Conservative
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TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: prote
FRAGMENT TYPE: intel
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LENGTH: 1165 amino aci
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; SEQ ID NO 1
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo s
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TITLE OF INVENTION: ASSAY SYSTEMS FOR LEF
FILE REFERENCE: REG 580-A
CURRENT APPLICATION NUMBER: US/09/093,814
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/049,108
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches 1164
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                                                                                                                                                                                                                                                                  atch 99.9%;
cal Similarity 99.9%;
1164; Conservative
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                                                                       SENSTTVIREADKIVSATSLLVDSILP 300
                                                                                                                                                                                     EQDRNCSLCADNIEGKTFVSTVNSLVF 120
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         PNLNETKPRGKFTYDAVYCCNEHECHH 420
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RESULT 4
US-08-618-957A-11
; Sequence 11, Application US/08618957A
; Patent No. 6355237
; GENERAL INFORMATION:
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                                                APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cloffi, Joseph
APPLICANT: Cloffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING TH
TITLE OF INVENTION: GENE AND ITS GENE PH
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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ADDRESSEE:
STREET: 11:
CITY: New '
STATE: NY
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                           TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.9%;
Best Local Similarity 99.9%;
Matches 1164; Conservative
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CURRENT APPLICATION NUMBER: US/08/6
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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                                                      RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480
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Patent No.
GENERAL IN
APPLICANT: Snodgrass, H. R.
APPLICANT: Snodgrass, H. R.
APPLICANT: Cloffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE
TITLE OF INVENTION: RECEPTOR IN REPRO
INUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.7%;
Best Local Similarity 99.1%;
Matches 1155; Conservative
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
                                                                                    PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV
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        GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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GASVANFNLTESWPMSKVNTVQSLSAYPLNSS
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TVIVSWILSPSDYKLMYFIIEWKNLNED
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RESULT 6
US-08-618-957A-8
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                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08618957A Patent No. 6355237 GENERAL INFORMATION:
                                                                                                          COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION TIPORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 008907-0033-999
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cloff1, Joseph
APPLICANT: Zupanclc, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE
TITLE OF INVENTION: GENE AND ITS GENE PH
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1141
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STREET: 1155 Avenue of The &
CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
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NAME: Poissant, Brian M.
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CORRESPONDENCE ADDRESS:
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STREET: 1155 Av
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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TELEPAX: (212) 869-9741/8864
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Cioffi, Joseph
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Hu-Bl.219,
RECEPTOR
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US-08-693-697-8
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                                                                                                                                                                                                                                                                                                     Patent No. 5869610
GENERAL INFORMATION:
                                                      STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Ver.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                            APPLICANT: Zupancic, Thomas J. APPLICANT: Shafer, Alan W. TITLE OF INVENTION: Hu-Bl.219, TITLE OF INVENTION: RECEPTOR
          APPLICATION NUMBER: US/08/693,697 FILING DATE: 05-AUG-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Cioffi, Joseph
INFORMATION:
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REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-697-8
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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nilarity 94.1%;
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Pred. No. 0;
7; Mismatches
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US-08-640-389A-3
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
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Patent No. 5912123
GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 901; Conservative
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STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Doissent Brian M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zupancic, Thom APPLICANT: Shafer, Alan W TITLE OF INVENTION: DETECTITLE OF INVENTION: RECEPTITLE OF INVENTION: REGUL NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: proto
)8-640-389A-3
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C, Thomas
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RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS
REGULATING REPRODUCTIVE BIOLOGY
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Pred. No. 0;
7; Mismatches
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FRNYNYKVHLLYVLPEVLEDSPLVPQKGS 180
                                                                  RSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
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RESULT 10
US-08-693-696-8
; Sequence 8, Application US/08693696
; Patent No. 6005080
; GENERAL INFORMATION:
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APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Ame
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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APPLICATION NUMBER: US 08/355,

FILING DATE: 14-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 7225-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Ma
Best Loc
Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
                                                               483
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Local Similarity 94.1%;
les 901; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCL
                                                             PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWI
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                    SSVKAEITINIGLLKISWEKPVFPENNLQFQIR
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                     RYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
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                                                              RINHSLGSLDSPPTCVLPDSVVKPLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 960;
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RESULT 11
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                                                                                                                                               NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
RELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
Query
Best I
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                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Snodgrass, H. R.
APPLICANT: CIOITI, Todeph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                           MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 11
CITY: New
STATE: New
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                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
Local
               Match
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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ESSEE: Pennie & Edmonds
ET: 1155 Avenue of the Ar
  Similarity
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RESULT 12
US-08-588-190-3
; Sequence 3, Application U
; Patent No. 5856098
; GENERAL INFORMATION:

US/08588190

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

WI: Snodgrass, H. R WI: Cloffi, Joseph WI: Zupancic, Thomas WI: Shafer, Alan Way INVENTION: DETECT

Thomas Joel

Ralph

Alan Wayne DETECTION

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RECEPTOR

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
08-588-190-3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 18-JAN-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
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STREET: 1155 A
CITY: New York
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                                                                     LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP
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pred. No. 0;
7; Mismatches
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                                                                                                                                    COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2
CURRENT APPLICATION NUMBER: US/08/6
                                                                                                                                                                                                                                 STREET: Pennie & I
STREET: 1155 Avenue c
CITY: New York
STATE: NY
COUNTRY: USA
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                                ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                    FILING DATE: 20-MAR-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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Shafer, Alan Wayne
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PRODUCT TO STIMULATE HEMATOPOIETIC
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Best Local Similarity
Matches 900; Conser
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
08-618-957A-3
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               GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
                                               VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQK
                                                                                TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
                                                                                                               FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPPFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSVQPINMVKPDPP
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7; Mismatches
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RESULT 14
US-08-618-957A-10
; Sequence 10, Applicatic
; Patent No. 6355237
; Patent No. FORMATION:
                                                                                                                                                                                                                                                                    ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-618-957A-10
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americ
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,95
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 28,462
REFERENCE/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 99.7%;
Matches 888; Conservative
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APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING
TITLE OF INVENTION: GENE AND ITS GENE
TITLE OF INVENTION: DEVELOPMENT
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CORRESPONDENCE ADDRESS:
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6355237
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Pred. No
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RESULT 15
US-08-693-697-36
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APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Cioffi, Joseph
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.21:
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmond:
STREET: 1155 Avenue of the
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M:
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RECEPTOR
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        PC-DOS/MS
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
JS-08-693-697-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: Amino acids
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Best Loc
Matches
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                                                                                         541
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Local Similarity 99.7%;
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                      PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVV
                                 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVV
                                                                   SSVKAEITINIGLLKISWEKPVFPENNLQFQIR
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Pred. No. 0;
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B219/OB RECEPTOR ISOFORM
7; 6D51126F33076626 CRC64
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutherla; Primates; Catarrhini; Hominidae;
NCBL_TaxID=9606;
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Novel B219/OB receptor isoforms: possible rol hematopoiesis and reproduction.";

Nat. Med. 2:585-589(1996).

EMBL: U52913; AAC50510.1; -.

HSSP; P16471; 1BP3.

InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN_III.

InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003531; Hematopo_receptor_S_F1.
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InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
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MEDLINE-96206; PubMed-8616721;
Cloffi J.A., Shafer A.W., Zupancic T. Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms: poshematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
EMBL; U52914; AAC50511.1; -...
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01-DEC-2001 (TrEMBLrel, 19, Last 8 B219/OB RECEPTOR ISOFORM HUB219.3 Homo sapiens (Human).
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Murinae; Mus
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STRAIN-KK OBESE; TISSUE-BRAIN, HYPOTHALAMUS;
Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg
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Sciurognathi; Muridae;
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Last annotation update)
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"Hyperleptinemia and leptin receptor variant Ashyperinsulinemic KK mouse strain.";
J. Endocrinol. 21:337-345(1998).

EMBL; Y10296; CAA71342.1; -...

HSSP; P16471; 1BP3.

MGD; MGI:104993; Lepr.

InterPro; IPR002996; CR1A.

InterPro; IPR003961; FN_III.

InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003531; Hematopo_receptor_S_F1.

Pfam; PF00041; fn3; 3.

CMART: SM00060; FN3; 3.
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Rest Local Similarity 75.3%; Pred. No. 0;
Matches 878; Conservative 116; Mismatches
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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Q9QWG3;
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01-MAY-2000 (TrEMBLrel. 13, L
01-DEC-2001 (TrEMBLrel. 19, L
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TISSUE-ADIPOSE TISSUE;
MEDLINE-98408931; PubMed-9738551;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
"Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA expression in the adipose tissue of normal, hyperinsulinemic, and type 2 diabetic rhesus monkeys.";
Obes. Res. 6:353-360(1998).
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Q9MYK9
ID Q9MYK9,
AC Q9MYK9;
DT 01-OCT-2000 (TrEMBLrel, 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel, 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
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TISSUE=ADIPOSE TISSUE;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

R HSSP; P16471; 1BP3.
R HSSP; P16471; 1BP3.
R InterPro; IPR002996; CR1A.
R InterPro; IPR003961; FN_III.
R InterPro; IPR003529; Hematopo_receptor_L_F2.
R InterPro; IPR003531; Hematopo_receptor_S_F1.
R Ffam; PF00041; fn3; 2.
R SMART; SM00060; FN3; 1.
R PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
R PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
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Best Local Similarity 95.0%; Pred. No. 0;
Matches 850; Conservative 15; Mismatches
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O9MYL1
O9MYL1;
O9MYL1;
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 19, Last annotation update)
LEPTIN RECEPTOR SHORT ISOFORM.
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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puence, tissue distribution,
of normal, hyperinsulinemic,
                                                                                                                                                                                                                                                                  KLFWEDVPNPKNCSWAQGLNFOKPETF
                                                                                                                                                                                                                                                                           KLFWEDVPNPKNCSWAQGLNFQKIRGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-ADIPOSE TISSUE;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodki
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF225873; AAF35387.1;
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;

MEDLINE-98408931; PubMed-9738551;

Hotta K., Gustafson T.A., Ortmeyer I.

Monkey leptin receptor mRNA: sequerexpression in the adipose tissue of 2 diabetic rhesus monkeys.";

Obes. Res. 6:353-360(1998).
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PISKPKDCYLQSDGFYECVFQPIFLLSG
                                                                                                                                                                                     GASVANFNLTFSWPMSKVNIVQSLSAYP
                                                                                                                                                                                                                                                                           GLYVIVPVIISSSILLIGTLITCHQRMK
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PROSITE; PS01353; HEMATOPO_REC_L_I
PROSITE; PS01355; HEMATOPO_REC_S_I
                                                                                                                                                                                                PISEPKDCYLQSDGFYECIFQPIFLLSG
                                                                                                          PDLCAVYAVQVRCKRLDGLGYWSNWSNP
                                                                                                                   GLYVIVPVIISSSILLLGTLLISHQRMK
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                                          #ICOKFCVVLLHWEFICVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNL
                                                                    SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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|SSVKAEIIKNIGLLKISWEKPVFPENNLQFQIRYGLSGKEIQWKMYDVYDAKSKSVSLPV
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                                  MICQKFCVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNT
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Length
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09MZS2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).
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 B
       ed. No. 0;
Mismatches
Score 4590;
Pred. No. 0,
73.4%;
larity 95.3%;
Conservative 15
        Local Similarity
es 849; Conser
Query Match
Best Local S
Matches 849
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                   Euteleostomi;
Sus,
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                   ata; Vertebrata;
; Suina; Suidae;
                                                                                                                                                                                                                                                          3970.5; DB 6;
No. 6.9e-285;
smatches 69;
                                                                                                                                                                                   UNKNOWN_1.
                                                                                 Cloning of
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                                                                                                                                                                                                                                                                             Mismatches
                                                                              "Expression, Detection, and Partial Cl (OBR) Gene.";
Submitted (JUL-1999) to the EMBL/GenBa EMBL; AF167719; AAF89633.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor InterPro; IPR003531; Hematopo_receptor Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
PROSITE; PS01353; HEMATOPO_REC_LF2; IPROSITE; PS01355; HEMATOPO_REC_LF2; IPROSITE; PS01355; HEMATOPO_REC_LF2; IPROSITE; PS01355; HEMATOPO_REC_S_F1; IPROSITE STATES
   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Crani:
Mammalia; Eutherla; Cetartiodactyla
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                      300 VQVRGKRLDGPGIWSDWSTPFTFTQDVIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
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LRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDAGLYVI
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STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
Wang M.-Y., Unger R.H.;
"Characterization of leptin receptors in normal and
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Interpro; IPR002996; CRIA.
Interpro; IPR003529; Hematopo_receptor_L_F2.
Interpro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1 PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1
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Submitted (MAR-1996) to the
EMBL; U53144; AAB03088.1;
HSSP; P16471; 1BP3.
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01-NOV-1996
01-NOV-1996
01-DEC-2001
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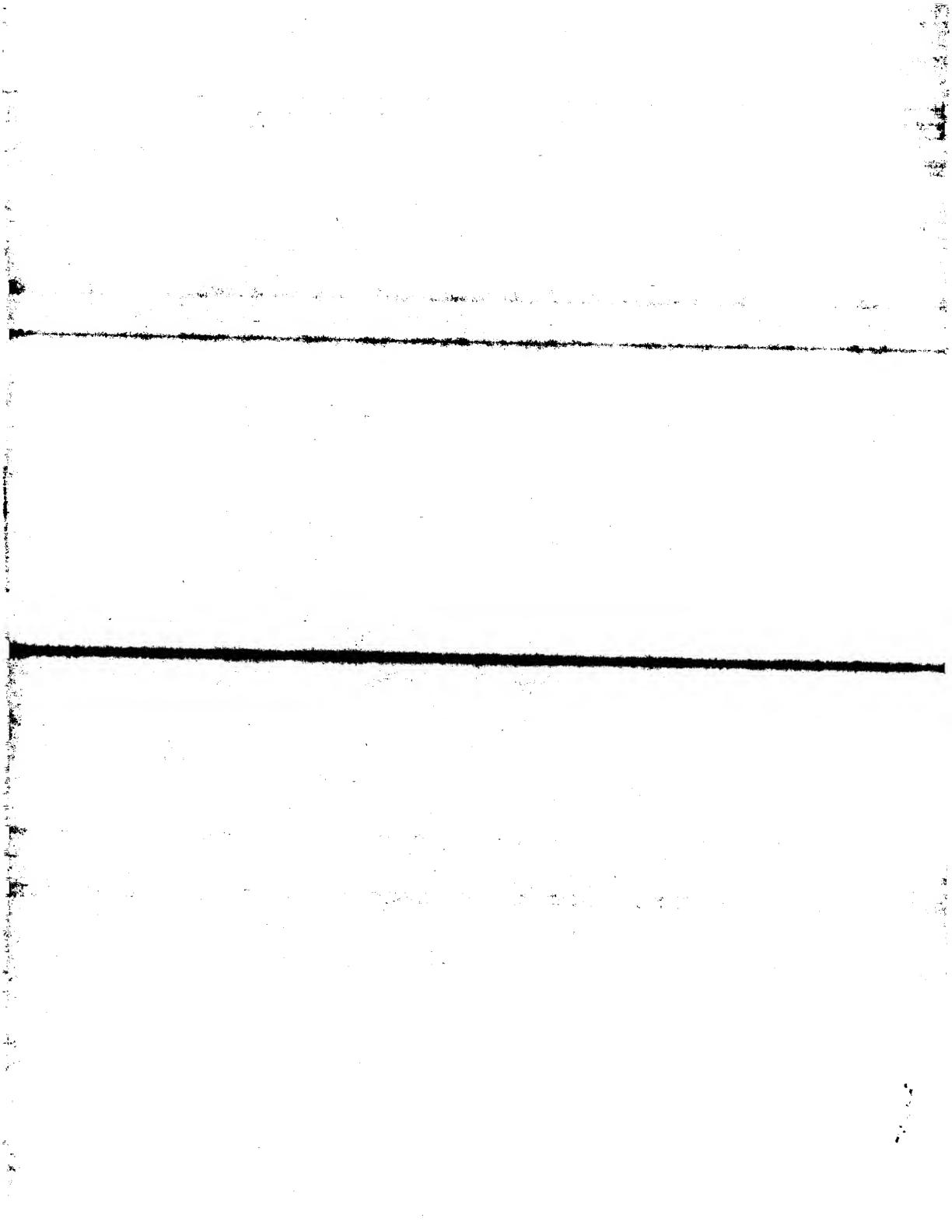
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lliformes; Meleagrididae; Meleagris
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LSSSCVILSWTLSPNDYSLLYLVIEWKNLNDD
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QVKYSENSTTVIREADKIVSATSLLVDSILP
          FQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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4197B7908F734F4 CRC64;
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enBank/DDBJ databases
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InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 4.
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Eukaryota; Metazoa; Chordata; Crani
Archosauria; Aves; Neognathae; Gall
NCBI_TaxID*9103;
                                                                                                                                                                                                                                                                      GASVANFNLTFSWPMSKVNIVQSLSAYPL
LGLHMEITDDGNLKISWSSPPLVPFPLQY
         RYAELYVIDVNINISCETDGYLTKMTCRW
                                                                                                           SSVKAEITINIGLLKISWEKPVFPENNLO
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1147 AA;
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TISSUE-BRAIN;
Richards M.P., Poc
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01-DEC-2001
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                                                                                 VLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLP--AGLSKNTSNSNGHY
 Length
Score 2790.5; DB 13;
Pred. No. 1.9e-197;
); Mismatches 364;
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 44.6%;
larity 48.6%;
Conservative 190
 Query Match
Best Local Similarity
Matches 566; Conser
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Search completed: August 15, 2002, 16:35:36 Job time: 796 sec



us-08-779-457-2.rsp



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 15, 2002, 16:24:10;

Run on:

Search time 28.14 Seconds (without alignments) 1602.995 Million cell updates/sec

Title: Perfect score: Sequence:

.....QTCSTQTHKIMENKMCDLTV 1165 US-08-779-457-2 6254 1 MICQKFCVVLLHWEFIYVIT.

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:1 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		 sapien	norv	CO.	musculu	sapien	norv	musculu	apien	Sapien	musculu	sapien	a liv	musculu	gall	ıris g	is lae	musculu	sapien	sapien	; gall	hila	nromis	ısculu	s norv	sapien	musculu	norv	norv	ı mula	apien	norv	hila	, O
	ription		rattu	SIL	RUS	homod	rattu	mus	уошоц	homo	Bus	homo	colu	mus	594 gallus gal	094 meleac	740 xenopus	mus	ношо	859 homo s	gallu	621 drosog	513 oreochromis	211 mus musculu		homod	mus	603 rattus	710 rattus	194 macaca	715 homo sapien	937	241 drosophila	7.00
	Des	P48	062	P48	000	P40	P40	P40	P42	660	P42	660	060	P97	004	091	091	P97	090	092	060	P16	160	P70	P22	P02	P22	P97	P05710	P79	.660	9	P20	oc C
	ID	LEPR_HUMAN	LEPR RAT	LEPR_MOUSE	IL6B_MOUSE	IL6B_HUMAN	IL6B_RAT	GCSR_MOUSE	LIFR_HUMAN	GCSR_HUMAN	LIFR_MOUSE	I12S_HUMAN	PRLR_COLLI	I12S_MOUSE	PRLR_CHICK	PRLR_MELGA	FINC_XENLA	NEO1_MOUSE	DSCA_HUMAN	NEO1_HUMAN	NEO1_CHICK	LAR_DROME	PRLR_ORENI	DCC_MOUSE	IL6A_RAT	FINC_HUMAN	IL6A_MOUSE	NEO1_RAT	PRLR_RAT	GHR_MACMU	CA1C_HUMAN	FINC_RAT	NRG_DROME	ים מפר מי זממ
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DCC_HUMAN	GHR_HUMAN	S230_PLAFO	PRLR_BOVIN	IL3B_MOUSE	GHR_PIG	GHR_RABIT	TPOR_HUMAN	PTPF_HUMAN	FINC_BOVIN	PMP9_CHLPN	EPA5_CHICK
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ALIGNMENTS

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                                                                         Hinney A., Ziegler A., Kunz J., I J., Grzeschik K.-H.; sequence variants at the leptin German children and adolescents
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ott J., Aitman T.J.;
nd obesity: lack of asso
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LEPTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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FIBRONECTIN TYPE-III 3.
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
Pfam; PF00041; fn3; 2.
SMART; SM00060.
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VARIANTS ARG-109; ARG-223; ASN-656 P
WEDLINE-99075638; PubMed-9860295;
Roth H., Korn T., Rosenkranz K., Hir
Slegfried W., Mayer H., Hebebrand J.
"Transmission disequilibrium and secreceptor gene in extremely obese General Genet. 103:540-546(1998).
                                                                                                                                              MEDLINE-97318795; ARG-223 AND ASN-69
MEDLINE-97318795; PubMed-9175732;
Gotoda T., Manning B.S., Goldstone &
Strosberg A.D., McKeigue P.M., Scott
"Leptin receptor gene variation and
white British male population.";
Hum. Mol. Genet. 6:869-876(1997).
-1- FUNCTION: RECEPTOR FOR OBESITY E
-1- SUBCELLULAR LOCATION: Type I men
-1- SIMILARITY: BELONGS TO THE CYTOP
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"Structure and sequence variation
lean and obese Pima Indians.";
jum. Mol. Genet. 6:675-679(1997).
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Obesity; Receptor;
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Best Local Similarity 99.9%;
Matches 1164; Conservative
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tation found in the Zucker fatty
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dugan V., Hey P.J., Caskey
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STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
MEDLINE-96295531; PubMed-8702432;
Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M.
"Substitution at codon 269 (glutamine --> proline) of treceptor (OB-R) cDNA is the only mutation found in the (fa/fa) rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Leptin receptor precursor (LEP-R) (OB receptor) (OB-R)
LEPR OR OBR OR FA.
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195; Q63385;
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Q62959; Q63007; P70493; P70494; P704
P97589; Q35772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 224:
                                                                     GLYVIVPVIISSSILLLGTLLISHQRMKKL
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STRAIN-SPRAGUE-DAWLEY, AND ZUCKER I
MEDLINE-96332408; PubMed-8769097;
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Nat. Genet. 13:18-19(1996).
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"Theretype of fatty due to Gln269Pro mutation in the leptin receptor (Lepr).";

Labeles 45:1141-1143(1996).

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Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
Mori K., Tamura N., Hosoda K., Nakao K.;
"Molecular cloning of rat leptin receptor isoform complementary
DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
MEDLINE-96212906; PubMed-8630068;
Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
"Phenotype-linked amino acid alteration in leptin receptor cDNA from zucker fatty (fa/fa) rat.";
Biochem. Biophys. Res. Commun. 222:19-26(1996).
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MEDLINE-96314329; PubMed-8690163;
Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
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                                                                                                                                                                                                                 SEQUENCE FROM N.A. (VARIANT B).
Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.
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Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polis Bell G.I.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          Carlsson B.; "Cloning of the rat leptin receptor."; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-123 FROM N.A.
Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
"Analysis of rat leptin receptor gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a leptin receptor in islet.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                       Biochem. Biophys. Res. Commun. 225:75-83(1996)
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EMBL; D84550; BAA12697.1; -.
EMBL; D84551; BAA12698.1; -.
EMBL; D85557; BAA12830.1; -.
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LEPTIN RECEPTOR.

EXTRACELLULAR (POTENTIAL).
POTENTIAL.

CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ..
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Glycoprotein;
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Best Local Similarity 75.6%;
Matches 882; Conservative 11
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                                                   GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J., Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J., Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S., Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I., "Identification and expression cloning of a leptin receptor, OB-R."; Cell 83:1263-1271(1995).
                                                                                                                                                                                                                                                                                                                                                                                                          Carroll K.M., Darvishzadeh J.G.,
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SEQUENCE FROM N.A. (VARIANT B).
STRAIN-C57BL/KSJ; TISSUE-Hypothalamus;
MEDLINE-96190816; PubMed-8608603;
Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
Duyk G.M., Tepper R.I., Morgenstern J.P.,
"Evidence that the diabetes gene encodes the leptin receptor;
"Evidence that the diabetes gene encodes the leptin receptor;
                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxiD=10090;
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STRAIN=C57BL/KS; TISSUE=Hypothalamus;
MEDLINE=96231997; PubMed=8628397;
Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadel
Lee J.I., Friedman J.M.;
"Abnormal splicing of the leptin receptor in diabetic mice.";
Nature 379:632-635(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (VARIANT C).
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=96206286; PubMed=8616721;
Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
Mikhail A., Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (VARIANTS A AND B).
STRAIN-FVB/N; TISSUE-Spleen;
MEDLINE-96270520; PubMed~8692797;
Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
             (B219
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receptor) (OB-R)
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Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igel M., Becker W., Herberg L., Joost H.G.; "Hyperleptinemia, leptin resistance, and poin the New Zealand obese mouse."; Endocrinology 138:4234-4239(1997).
01-MAR-2002 (Rel. 41, Last annotation
Leptin receptor precursor (LEP-R) (OB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chua S.C., Koutras I.K., Han L., Liu
Chung W.K., Leibel R.L.;
"Fine structure of the murine leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            suppression is required to form two
transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - FUNCTION: RECEPTOR FOR OBESITY
                                                                                                                      TISSUE-Choroid plexus;
MEDLINE-96128129; PubMed-8548812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (VARIANT B).
STRAIN-NEW ZEALAND OBESE / NZO; T
MEDLINE-97462708; PubMed-9322935;
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                                                                                                             SEQUENCE FROM N.A. (VARIANT A).
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-!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN

TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT

E) COULD FUNCTION AS A TRANSPORT PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
WHICH COULD BE SECRETED.

-!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN
LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.

(2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND
LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:
EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.

-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                     EXPRESSION IN
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R EMBL; 049106; AAC32420.1; --
R EMBL; 049106; AAC32420.1; --
R EMBL; 049106; AAC32420.1; --
R EMBL; 049108; AAC32420.1; --
R EMBL; 049109; AAC32409.1; --
R EMBL; 049109; AAC32409.1; --
R EMBL; 049109; AAC322706.1; --
R EMBL; 058863; AAC32706.1; --
R EMBL; 058863; AAC32706.1; --
R EMBL; 058863; AAC32706.1; --
R EMBL; 058863; AAC323706.1; --
R EMBL; 0589443; AAB95334.1; JOINED.
R EMBL; 05939446; AAB95334.1; JOINED.
R EMBL; 0593946; AAB95334.1; JOINED.
R EMBL; 0593940; AAB95334.1; JOINED.
R EMBL; 0703943; AAB95334.1; JOINED.
R EMBL; 0703943; AAB95334.1; JOINED.
R EMBL; 0703943; AAB95334.1; JOINED.
R EMBL; 0703945; AAB95334.1; JOINED.
R EMBL; 0703945; AAB95334.1; JOINED.
R EMBL; 0703945; PAUBS; 0500000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 050000; 05000; 050000; 05000; 050000; 05000; 05000; 05000; 050000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 050000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 05000; 0
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LEPTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
N-LINKED (GLCNAC. . .) (POT
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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No. 0;
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llarity 75.4%;
Conservative 115
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NUCLIARALD-10090;

NEDLINE-92291532; Pubmed-1602143;

SEQUENCE FROM N.A.

SEQUENCE TISSUE-Macrophage;

NA Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;

MEDLINE-92291532; Pubmed-1602143;

A Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;

Transducer, gpl30, and its regulated expression in vivo.";

Transducer, gpl30, and its regulated expression in vivo.";

Transducer, gpl30, and its regulated expression in vivo.";

I. FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, ONTF, AND IL-11 CAN UTILIZE GPl30 FOR INITIATING SIGNAL TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.

C. I. SUBCELLULAR LOCATION: TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
6 signal transducer) (Membrane glycoprotein 130) (GP130).
IL6ST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Sciurognathi; Muridae; Murinae; Mus
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Homo sapiens (Human).
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IL6B_HUMAN
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
     STEM CELLS IT IS FOUND FROM DAY ON DAY 8 AND GRADUALLY DECLINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONVYGVTMLSGFPPDKPTNLTCIVNEG--KNMLCOWDPG-----RETYLETNYTLKSEWA 165
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                                                                                                                                                                                                                                                         Signal;
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                                 C2-TYPE DOMAIN.
DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND 16 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY 1 DURING THE REST OF EMBRYOGENESIS.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                        in; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 917;
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KE C2-TYPE DOMAIN.

NECTIN TYPE-III 1.

NECTIN TYPE-III 2.

NECTIN TYPE-III 3.

NECTIN TYPE-III 4.
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Pred. No. 5.9e-17;
1; Mismatches 338;
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InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003529; Hematopo_receptor
Pfam; PF00041; fn3; 4.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 2.
PROSITE; PS01353; HEMATOPO_REC L F2: 1
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EMBL; M83336; AAA37723.1;
HSSP; P40189; 1BQU.
MGD; MGI:96560; Il6st.
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SDIPSIHPISEPKDCYLQSDGFYECI - - FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLP
                                  ----WKMYEVYDAKSKSVSLPVPDL--CAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMD
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                                                                                                                                                                      --VSSGLGGLLDLKSDIQYRT
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                                                                                                              532 DSVVKPLPPSSVKAEITINI-GLLKISWEKPVFPENNLQFQIRYGLSG----KEVQ---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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P40189; Q9UQ41;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-6 receptor beta chain precursor (IL-6R-beta)
6 signal transducer) (Membrane glycoprotein 130) (GP130)
receptor) (CDw130) (CD130 antigen).
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                                                                                                                                            215 VDKVKPTPPYNLSVTNSEELSSILKLSW-
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TISSUE*Myeloma, and Placenta;
MEDLINE=91084844; PubMed=2261637;
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ein; Immunoglobulin domain; Signal;
splicing.
                                                                                                                                                         PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES. MEDLINE-21269388; PubMed-11098061; Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.; Determination of the disulfide structure and N-glycosylation sites the extracellular domain of the human signal transducer gpl30."; J. Biol. Chem. 276:8244-8253(2001).
                                                                                          Okubo
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Kishimoto T
transducer,
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o T., Taga T.,
an IL-6 signal
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InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR003529; Hematopo_recept
Pfam; PF00041; fn3; 3.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 3.
                                                                                       Tanaka M., Kishimura M., Ozaki S., O Murakami M., Nakao K.; "Cloning of novel soluble gpl30 and autoantibodies in rheumatoid arthrit J. Clin. Invest. 106:137-144(2000).
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Receptor; Transmembrane; Glycoprot:
Repeat; 3D-structure; Alternative :
SIGNAL 1 22
CHAIN 23 918 INTER:
DOMAIN 23 619 EXTRA
                                                      SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE-Synovium;
MEDLINE-20341529; PubMed-10880057;
   "Molecular cloning and expression gp130.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M57230; AAA59155.1; -
EMBL; AB015706; BAA78112.1;
PIR; A36337; A36337.
PDB; 1BQU; 26-AUG-98.
Saito
                                Cell 63:1149-1157(1990).
Murakami M.,
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sKA -> NIASF (IN GP130-RAPS)
sSING (IN GP130-RAPS).
D813F3672DD10D53 CRC64;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
SER-RICH.
BY SIMILARITY.
BY GICCNAC...) (POT N-LINKED (GLCNAC...)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%; Score 339.5; DB 1;
larity 20.8%; Pred. No. 3.7e-15;
Conservative 141; Mismatches 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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ctor receptor precursor (G-CSF-R)
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MEDLINE-97331327; PubMed-9187659;

MEDLINE-97331327; PubMed-9187659;

Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;

Tolution structure of an extracellular domain containing the WSxW solution structure of an extracellular domain containing the WSxW motif of the granulocyte colony-stimulating factor receptor and it interaction with ligand.";

Nat. Struct. Biol. 4:498-504(1997).

-i- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR.

ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENT THE CELL SURFACE.

-i- SUBCELLULAR LOCATION: Type I membrane protein.

C-i- SUBCELLULAR LOCATION: Type I membrane protein.

C-i- SUBCELLULAR LOCATION: Type I membrane protein.

C-i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

C-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

C-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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Murinae; Mus
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llular domain containing the WS
timulating factor receptor and
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Sclurognathi; Muridae;
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01-FEB-1995 (Rel. 31, Last sequenc
30-MAY-2000 (Rel. 39, Last annotat
Granulocyte colony stimulating fac
CSF3R OR CSFGR.
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MEDLINE-90235283; PubMed-2158861;
Fukunaga R., Ishizaka-Ikeda E., St
"Expression cloning of a receptor stimulating factor.";
Cell 61:341-350(1990).
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een the Swiss Institute of Bi
European Bioinformatics Instit
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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PDB; IGCF; 22-OCT-97.

PDB; ICTO; 22-OCT-97.

MGD; MGI:1339755; Csf3r.

InterPro; IPR002996; CR1A.
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IG-LIKE C2-TYPE DOMAIN.
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
Receptor; Transmembrane; Glycoprotein; Immur
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GRANULOCYTE
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KLMYF1IEWK----NLNEDGE1KWLR1SSSVKKYYIHDHF1P1EKYQFSLYP1FMEGVGK

Thu Aug 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta;

TISSUE-Placenta;

We dearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,

King J., Price V., Cosman D., Beckmann M.P.;

Leukemia inhibitory factor receptor is structurally related to the in-

T.E.6 signal transducer, gpl30.";

EMBO J. 10:2839-2848(1991).

- I- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY WITH GPl30. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF LIFE SUBUNIT: HETERODIMER COMPOSED OF LIFER AND GPl30.

- I- SUBUNIT: HETERODIMER COMPOSED OF LIFER AND GPl30.

- I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.

- COURTINE BY ALTERNATIVE SPLICING.

- I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

- I- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

- I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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----PSRTGDQVLYGQVLESPTSPGVM 766
- PTIMTEET----FQLPSFW-----DSSVPSITKITELEEEDKKPTHWDSESSGNGSLP
                                                                                      PVNVYTFAGERAPPHAPALHLKHVGTTWAQLEWVPEAPRLGMIPLTHYTIFWADAGDHSF
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                                                                                                                         --VIVPV
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Catarrhini; Hominidae; Homo.
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01-NOV-1995 (Rel. 32, Last sequence
16-OCT-2001 (Rel. 40, Last annotation
Leukemia inhibitory factor receptor
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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825 GLQVHGVEE----QGGF 837
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                                                                                                                                                                                                                                                                                            POTENTIAL.
LEUKEMIA INHIBITORY FACTOR RECEPTOR
EXTRACELLULAR (POTENTIAL).
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BY SIMILARITY.

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llarity 19.2%; Pred. No. 5.3e-12;
Conservative 179; Mismatches 385;
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                                                              InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
Receptor; Transmembrane; Glycoprotein; Immunog Alternative splicing; Repeat.
SIGNAL 1 44 POTENTIAL.
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                                                                                                                                                               ---QAKPEEEQENDPVGGAGYKPQMHLPINSTVEDIAAE
                                                                                                        -GKNLIIYWKPLPINEA----NGKILSYNVS
                                                                                                                                               CNG-----TWSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMSKVNIV
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                               VSLPVPDLCAVYAVQVRCKRLDGLGYWSNWS
                                                         -NSSYLVALDKLNPYTLYTFRIRCS-TETFWKWSKWS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        KEKNVTLLWKPLMKNDSLCSVQRYVINHHTS
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tor receptor precursor
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                                                                                      NPAYTVVMDIKVPMRGPEFWRIINGDTMK
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                               NLQFQIRYGLSGKEVQWKMYEVYDAKSKS
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MEDLINE-91079757; PubMed-2147944;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98037802; Pubmed-9368043;
Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;
MEDLINE-98037802; Pubmed-9368043;
Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;
"Identification of a ligand-binding site on the granulocyte colony-stimulating factor receptor by molecular modeling and mutagenesis.";
J. Biol. Chem. 272:29735-29741(1997).

-!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
EVENTS AT THE CELL SURFACE.

-!- SUBUNIT: DIMER (PROBABLE).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, THE GCSFR-2 FORM,
WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
WYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
-!- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;
ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
-!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD114 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".
                                                                   colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97331327; PubMed-9187659; MEDLINE-97331327; PubMed-9187659; MEDLINE-97331327; PubMed-9187659; Vamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.; Solution structure of an extracellular domain containing the WSXWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand."; Nat. Struct. Biol. 4:498-503(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE RECEPTOR,
ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; GCSFR-1 (SHOWN HERE),
GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY
ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
                                                                                                                                                                                                                                                                                                   DOMAINS STRUCTURE.
MEDLINE=92007729; PubMed-1717255;
Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;
"Functional domains of the granulocyte colony-stimulating factor
                                                                                                                                                                                                                    colony
                                                                                                                                                                      MEDLINE-92091782; PubMed-1530796;
Seto Y., Fukunaga R., Nagata S.;
"Chromosomal gene organization of the human granulocyte
stimulating factor receptor.";
J. Immunol. 148:259-266(1992).
Eukunaga R., Seto Y., Mizushima S., Nagata S.; "Three different mRNAs encoding human granulocyte factor receptor.";
                                                                                                           Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                          receptor.";
EMBO J. 10:2855-2865(1991).
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EMBL; X55720; CAA39252.1; -
EMBL; S71484; AAB20660.1; -
EMBL; M59818; AAA63176.1; -
EMBL; M59819; AAA63177.1; -
EMBL; M59820; AAA63178.1; -
PIR; JH0329; JH0329.
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                                                                                                              Proc. Natl. Acad.
                                                                                                                                                       SEQUENCE FROM N.
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                         HCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP
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Murinae; Mus
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STRAIN=ICR; TISSUE=Liver;
MEDLINE=94039833; PubMed=7901054;
Tomida M., Yamamoto-Yamaguchi Y., Hozumi M.;
"Pregnancy associated increase in mRNA for soluble D-factor/LIF
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MEDLINE=92007727; PubMed=1915266;
Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.
King J., Price V., Cosman D., Beckmann M.P.;
"Leukemia inhibitory factor receptor is structurally related
IL-6 signal transducer, gp130.";
EMBO J. 10:2839-2848(1991).
                                                                                                                                                                                                                                                                                                       -QRQLDPRTVQLFWKPVPLEEDSGRIQGYVVSWRPSGQAGAILPLCNTT--
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Sciurognathi; Muridae;
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MEDLINE-94334302; PubMed-8056772;
Tomida M., Yamamoto-Yamaguchi Y., Hozumi M.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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FEBS Lett. 334:193-197(1993).
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LIFR_MOUSE
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                                                                                                                                                                                                                                                                                      Immunoglobulin domain; Signal;
                                                                                                                                                                                                                                                                                                                                                 GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 5.

BY SIMILARITY.
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red. No. 1.8e-11;
Mismatches 287
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          PIR; JH0330; JH0330.
PIR; A38252; A38252.
PDB; 1A27; 28-JAN-98.
MIM; 138971; -.
MIM; 202700; -.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 2.
PROSITE; PS01353; HEMATOPO_REC_L_F2; 1
Receptor; Transmembrane; Glycoprotein; Repeat; Alternative splicing; 3D-struc SiGNAL
24 GRANULOCY
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   -LMSVQPINMVKPDPPLGLHMEITDD----GNLKISWSS-PPLVPF
                                 DHEVTINYLNGFQSKFTLNEKDVSLIPETPEI---LDLSADFFTSSLLLKWNDRGSALPH
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                                                                                                                                | :::| :| | :::| ::| | SNATWEIKVLONPRT ---EPVALVLLNTWLSGKDTVQHWNWTSDLPLQCATHSVSIRW-
                                                                                                                                                                                            --WSDWSTPRVFT---TQDVIYFPPKILTSVGSNVSFHCIYKKENKIVPS
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                                                                                               -- VDSILPGSSYEVQVRGK
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"Three different cDNAs encoding mouse D-factor/LIF receptor.";

J. Biochem. 115:557-562(1994).

-!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.

-!- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.

-!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS MAY ARISE BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN, AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF THE SECRETED FORM.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                                                   MOLECULE. MAY HAVE A COMMON PATHWAY INHIBITS THE BIOLOGICAL ACTIVITY OF TO RECEPTORS ON TARGET CELLS.
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EMBL; S73495; AAC60697.1; -.

EMBL; D26177; BAA04258.1; -.

EMBL; D17444; BAA04258.1; -.

EMBL; D17444; BAA04258.1; -.

MGD; MGI:96788; Lifr.

InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN_III.

InterPro; IPR003529; Hematopo_receptor_L_F2.

Pfam; PF00041; fn3; 4.

SMART; SM00060; FN3; 3.

Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signative splicing; Repeat.
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S II CYTOKINE FAMILY OF RECEPTORS
TIN TYPE III-LIKE DOMAINS.
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OSED OF AT LEAST IL12RB1 AND
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Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.
Gately M.K., Gubler U.;
"A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits.";
Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
-I- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH LOW AFFINITY.
-I- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH
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EUKIN-12 RECEPTOR BETA-2 CHAIN
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hini; Hominidae; Homo.
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CYTOPLASMIC (POTENTIAL).
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in; Signal; Repeat
                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-12 receptor beta-2 chain precursor
2) (IL-12R-beta2).
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HSSP; P40189; 1BQU.
MIM; 601642; -.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3.
PROSITE; PS01353; HEMATOPO_REC_L_F2; 1
Receptor; Transmembrane; Glycoprotein; SIGNAL 1 21 POTENTIAL
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Catarr
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SIMILARITY: BELONGS TO THE CLASS
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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090374;
01-NOV-1997 (Rel. 35, Created)
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MEDLINE=97098510; Pubbmed=8943050; Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y. Gately M.K., Gubler U.; "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits."; Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
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Murinae, Mu
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Sciurognathi; Muridae;
                                                                                                                                                                                                         WSSERHIHIPNGESP --- PEKPTIIKCRSPEKE-TFTCWWKP--
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                                                     RYGLSGKEVQWKMYEVYDAKSKSVSLPVPDLCAV
                                                                                                                                                                                                                                                                TSCNGTWSEDVGNHTKFTFLWTEQA---
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                           raniata; Vertebrata; Euteleostomi;
Columbiformes; Columbidae; Columba
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BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CYTOPLASMIC (POTENTIAL).
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FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
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;; HEMATOPO_REC_L_F1; 1.
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                    01-NOV-1997 (Rel. 35, Last sequence 15-JUL-1998 (Rel. 36, Last annotatio Prolactin receptor precursor (PRL-R)
                                                                                                               Columba livia (Domestic pigeon).
Eukaryota; Metazoa; Chordata; Cran.
Archosauria; Aves; Neognathae; Colu
NCBI_TaxID=8932;
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_rece
Pfam; PF00041; fn3; 4.
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"Cloning, expression, and mutation receptor.";
Endocrinology 135:269-276(1994).
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MEDLINE-94283267; Pubmed-7516866;
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HSSP; P16471; 1BP3,
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SMART; SM00060; FN3;
PROSITE; PS01352; HI
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SIMILARITY: C
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                             SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                          coprotein; Signal; Repeat.
OR 23 (POTENTIAL).
INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
EXTRACELLULAR (POTENTIAL).
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LOW AFFINITY.
SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL
AFFILITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
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FIBRONECTIN TYPE-111 1.
FIBRONECTIN TYPE-111 2.
FIBRONECTIN TYPE-111 3.
FIBRONECTIN TYPE-111 4.
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InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003529; Hematopo_receptor_L_F2
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larity 20.3%; Pred. No. 4.2e
Conservative 95; Mismatches
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PRINTS; PR00014; FNTYPEIII.

SMART; SM00060; FN3; 3.

PROSITE; PS01353; HEMATOPO_REC_LF2
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HSSP; P40189; 1BQU.
MGD; MGI:1270861; Ill2rb2.
InterPro; IPR002996; CRIA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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STRAIN-WHITE LEGHORN; TISSUE-Kidney;
MEDLINE-93075121; PubMed-1445292;
Tanaka M., Maeda K., Okubo T., Nakashima K.;
"Double antenna structure of chicken prolactin receptor deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cDNA sequence.";
Biochem. Biophys. Res. Commun. 188:490-496(1992).
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
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                                                             347 KODIDYDROOISLEWKSLNPSEARGKILHYQVTLOEVTKKTTLQNTTRHTS----WTRVI
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-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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PwaRT; SM00060; FN3; 3.
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PIR; JQ1655; JQ1655.
HSSP; P14787; 1AN3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
NCBI_TaxID=9103;
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Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-;-FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
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                   547 KETDSDSGRGSCDSPSLLSEKCRETCALPPVLQTQEVRDVQEKKAAKRSWET -- QYVASE
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EMBL; U22947; AAA75038.1; -
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JR EMBL; U22924; AAA75039.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003528; Hematopo_receptor_L_
DR InterPro; IPR003528; Hematopo_receptor_L_
DR SMART; SM00060; FN3; 3.
DR SMART; SM00060; FN3; 3.
DR ROCSTE; P601352; HEMATOPO_REC_L_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
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1 23 PROLACTIN RECEPTOR.
24 831 PROLACTIN RECEPTOR.
24 839 PROLACTIN TYPE-III 1.
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1 23 PROLACTIN TYPE-III 1.
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Matches 159; Conservative 126; Mis
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qq	: 484 E	: : : : : : : : : : :	518
δ	786 1	786 LRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDAG	841
qq	519 L	LEVEDSEDHQLMPSHDSGRPSKNAKITLKETDRDSGRGSCDS-	560
ΟŅ	842 I	LYVIVPVIISSILLLGTLLISHQRMKKLFWEDVPNP	878
QΩ	561 -	:: PSLLSEKCRETCALPSALQIQDVRDVQAKKAGKRSWESYCVASERKALLFNNESA	615
ŏ	879 K	JEIKHTASVTCGPLLLEPE	923
qa	616 K	KSSTWPAVQLPNNQPPTFAYHSIVEANKITSTTTNMNVAAVLVENEERHQSLYSISETIS	675
δy	924 -		962
qq	929	GGMEKQEEMENLHSKTTQTTVQVRQNRSNEKLPFLNAALMDYVEVHKVRQDEEPTVL	732
δy	963 -	-NFSEAEGTEVTYEDESOROPFVKYATLISNSKPSETGE 1000	1000
đ	733 1	LKHKEKSGKIEKYTISGASKEYTKVSTVMNHNILVLMPDSRVLHTPTSQEEPAKETSQNP 792	792
δy	1001 E	EQGLINSSVTKCFSS 1015	
qq	793 C	OGGOVETNMSYCMTA 807	

completed: August 15, 2002, 16:36:09 ne: 719 sec Search com Job time:

Compugen Ltd rsion 4.5 2000 Comp GenCore ver Copyright (c) 1993 - 2

protein search, using sw model OM protein Search time 54.95 Seconds (without alignments) 2037.199 Million cell updates/sec : 00 August 15, 2002, 16:20: Run on:

US-08-779-457-2 6254 Title: Perfect score:

....QTCSTQTHKIMENKMCDLTV 1165 1 MICOKFCVVLLHWEFIYVIT. Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

esidues 283138 seqs, 96089334 Searched:

283138 arameters: Total number of hits satisfying chosen p

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summar

ies

PIR 71-1 Database

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predicted by chance to have a score of the result being printed, total score distribution, Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

SUMM

ES	Description	leptin receptor, 0	. ,	receptor,	receptor,	receptor,	receptor,	leptin receptor, s	glycoprotein 130 -	membrane glycoprot	interleukin-6 sign	granulocyte colony		granulocyte colony		differentiation-st	granulocyte colony	protein-tyrosine-p	prolactin receptor	prolactin receptor	titin - rabbit (fr	ac	hypothetical prote	- 1	frazzled gene prot			neogenin - chicken	protein-tyrosine-p	
SUMMARIES	ID	PC4184	568438	S68440	m	S68437	7422	S68441	149699	A36337	A44257	A34898	S17308	C38252	JH0329	JX0312	B38252	T14328	I50455	JQ1655	S20901	I38344	T19506	A43908	T13822	T08851	T43027	I20600	딘	
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dF	Query Match	76.5		9.09									4.7	4.6	4.5	4.5	4.4	4.0	3.5	•		3.0	•				•		2.7	•
	Score	4784.5	4766.5	3793	3785	3785	3729	3340	366	345.5	339.5	313	294.5	288.5	284	281.5	277	251.5	220	209.5	91	188	182.5	177	174	172	170	169.5		
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prolactin receptor	frazzled gene prot	neural cell adhesi	kinase-related pro	protein H19M22.1 [hypothetical prote	kinase-related pro	titin - rabbit (fr	fibronectin precur	interleukin-6 rece	interleukin-6 rece	prolactin receptor	prolactin receptor	prolactin receptor	hypothetical prote	lactogen receptor
151086	T13823	T30581	I48310	C88400	T32828	173957	146521	FNHU	JL0144	JL0145	A36116	A29884	A41070	F82884	A34631
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2.6	5.6	5.6	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.4	2.4	2.4	2.4
165	165	160	159	158	158	158	156	154.5	153,5	153.5	153.5	150.5	150.5	150.5	148.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Lippin receptor, 00-Rb rate
Cipates: Rattus morveques (Norway rat)
Cipates: Is Awar-1996 seaquence_revision 13-Mar-1997 #text_change 01-Dec-2000
CiAccession: JC4895; JC4896; JC4997; Pc4184; JC4797
CiAccession: JC4895; JC4896; JC4897; Pc4184; JC4797
Rickenden maker: JC4895; JC6895; JC4891; JE96
A; Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifit
A; Reference number: JC4895; MUD: 96332408
A; Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifit
A; Residence: JC4895; MUD: 9632540
A; Accession: JC4895
A; Accession: JC4895
A; Molecule type: mRNA
A; Residues: 1-180; ARDIT. <7A2>
A; Accession: JC4895
A; Accession: JC4897
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A; Residues: DBJD189558; NID: 9152641; PIDN: BAA12831.1; PID: 401013515; PID: 915
A; Accession: JC4897
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A; Residues: DBJD189559
A; Cross-references: DBJD189559
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A; Cross-references: DBJD189559
B; Idda M; Murkani, T.: Ishida, M; Mulecula type: mRNA
A; Residues: ID-766, G'. 1157-1158
A; Cross-references: DBJD189559
B; Idda M; MULECANI, T.: Ishida, M; MULECANI, Teceptor CDNA from zucker f
A; Molecule type: mRNA
A; Residues: B40-1124 <11D>
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A; Residues: B40-1144
A; Mulecule type: mRNA
A; Mulecule type: mRNA
A; Residues: B40-1144
A; Mulecule type: mRNA
A; Residues: B40-11
Ob-Rb - rat
leptin receptor,
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Length 1162; C:Comment: This receptor is obese-phenotype-linked mutanic; Genetics:
A; Gene: fa
C; Keywords: appetite; transmembrane protein
F; 840-860/Domain: transmembrane #status predicted <TMM>
F; 861-1162/Domain: intracellular #status predicted <INT> Score 4784.5; DB 2; Pred. No. 6.5e-303; 76.5%; 75.6%; Query Match Best Local 9

Local Similarity

Ma	Matches	882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;
ò	e r	FCVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 6
2 2	T 19	KEY VYLLHWEFLIVITALNLAY PISPWKFRLFCAPPSTTDDSFLSPAGVPNISS STAVEDKENSSGTHFSNISKTTEHCCERSEODRNCSICADNIECKTRVSTVNSIV
G 6	61	ASEALVEAKFNSTGIYVSELSKTIFHCCFGNEQGQNCSALTGNTEGKTLASVVKPLVF 12
\$ 6	121	DANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSF : : : :: :
O D D	181	FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
ô	241	LHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 30
QQ	240	
Oy Dp	301	GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360
6 4	361	2 -
3 8	421	VICCNEUACH SLYCSDIPSI
g 2	419	47
Oy Dp	481	PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Qy Db	541 539	SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
O.Y Db	601 599	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Oy Dp	661 659	TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Oy Dp	721	GASVANFNLTESWPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780 :
5 G	781	GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Š G	841	SSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPE : SCVLLLGTLLISHQRMKKLFWDDVPNPKNCSWAQGLNFQKPE
Οy	901	TASVICGPLELEPETISEDISVDTSWKNKDEMMPTTVVSLLSTT-DLEKGSVCI
QQ	899	KHAESVIFGPLLEPEPVSEEISVDTAWKNKDEMVPAAMVSLLLTTPDSTRGSICISDQC 958
0.y Db	959	NSVNFSEAEGTEVTYEDESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSP 1019
Qy Op	1020	LKDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYY 1079 : ::

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C.Species: Mus musculus (house mouse)

C.Species: Wus musculus (house mouse)

C.Species: IV-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000

C.Accession: S68438; S68441

R.Lee, G.H.; Proenca, R.: Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;

Nature 379, 632-635, 1996

A.;Title: Abnormal splicing of the leptin receptor in diabetic mice.

A.;Accession: S68437; MuD:96231997

A.;Accession: S68437; MuD:96231997

A.;Accession: S68438

A.;Status: nucleic acid sequence not shown

A.;Residues: 664-1162 <LEEI>

A.;Cross_reference number: EMBL:U49107; NID:91195486; PIDN:AAC52421.1; PID:91195487

A.;Cross_references: EMBL:U49107; NID:91195486; PIDN:AAC52421.1; PID:91195487

A.;Cross_references: EMBL:U49107; NID:91195492; PIDN:AAC52421.1; PID:91195493

A.;Status: nucleic acid sequence not shown; translation not shown

A.;Mote: nucleotide sequence not shown; translation not shown

A.;Motecule type: mRNA

A.;Status: nucleic acid sequence not shown; translation not shown

A.;Motecule type: mRNA

A.;Residues: 1795, GwcrvyLFMD <LEEZ>

A.;Cross_references: EMBL:U49110; NID:91195492; PIDN:AAC52424.1; PID:91195493

A.;Residues: Liss sequence from Re: tissue hypothalamus

A.;Motec: the nucleotide sequence from Re: tissue hypothalamus

A.;Motec: the nucleotide sequence from Re: tissue hypothalamus

A.;Motec: the sequence from splice form Re: sincluded to produce a complete sequence

C.;Coment:: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C.;Genetics:

A.;Gene: OB-Rb

C.;Keywords: alternative splicing; appetite
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                                                                                                                 Conservative
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VPSKEIVWWMLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH

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A;Gene: Ob-Rd C;Keywords: alternative splicing; appetite; transmembrane protein F;840-860/Domain: transmembrane #status predicted <tmm></tmm>	Query Match Best Local Similarity 76.8%; Score 3793; DB 2; Length 900; Best Local Similarity 76.8%; Pred. No. 1.4e-238; Matches 691; Conservative 83; Mismatches 124; Indels 2; Gaps	Qy 1 MICQKECVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60 	Qy 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120 	QY 121 QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS 180 	QY 181 FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240	Qy 241 LGLHMEITDDGNLKISWSSPPLVPFFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300	QY 301 GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360 	Qy 361 VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420 : :	Qy 421 RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480 	QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540	OY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600 	Qy 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660 	QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720	Qy 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780 	Qy 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFWEGVGKPKIINSFTQDDIEKHQSDA 840 	Qy 84Î GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI 900 	RESULT 4 S68439 leptin receptor, splice form Ob-Rc - mouse
QY 421 RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480 	OY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540	QY 541 SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600 	QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660	OY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720	Qy 721 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780	Qy 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840 : : :	QY 841 GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI 900	QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTT-DLEKGSVCISDQF 959 	Qy 960 NSVNFSEAEGTEVTYEDESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSP 1019 	QY 1020 LKDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYY 1079 [: :	OY 1080 LGVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA 1139 : : :	Oy 1140 SYMPOFOTCSTOTHKIMENKMCDLTV 1165 	η (mouse) mouse) evision 17-Jul-1998 #text_change 31-Dec-2000	Riber, G.m.; Fidenca, R.; Montez, J.M.; Carroll, N.M.; Darvishzagen, J.G.; Lee, J.L.; Fr Nature 379, 632-635, 1996 A;Title: Abnormal splicing of the leptin receptor in diabetic mice. A;Reference number: S68437; MUID:96231997	not not	ypothalamus was submitted to the EMBL Data Library, Feb ce forms, see PIR:S68437, PIR:S68438, PIR:S6

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C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-2000 faequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C; Date: 31-Dec-2000 faequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C; Accession: S68439; S68441
R; Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fr
Nature 379, 632-635, 1996
A; Title: Abnormal splicing of the leptin receptor in diabetic mice.
A; Reference number: S68437; MUID:96231997
A; Accession: S68439
A; Residues: 664-892 cLEE1>
A; Residues: 664-892 cLEE2>
A; Molecule type: mRNA
A; Residues: 1-796, GMCTVLEMD' cLEE2>
A; Cross-references: EMBL: u49110; NID:91195492; PIDN:AAC55424.1; PID:91195493
A; Residues: 1-796, GMCTVLEMD' cLEE2>
A; Cross-references: EMBL: u49110; NID:91195492; PIDN:AAC55424.1; PID:91195493
A; Residues: 1-796, GMCTVLEMD' cLEE2>
A; Cross-references: EMBL: u49110; NID:91195492; PIDN:AAC55424.1; PID:91195493
A; Residues: 1-796, GMCTVLEMD' clee2>
C; Comment: For alternative splice form Re: sissue hypothalamus
A; Residues: Rom aplice form Re: sissue produce a complete sequence
C; Comment: For alternative splice forms, see PIR:S68437, PIR:S68439, PIR:S684639, PIR:S68-CC C; Reywords: alternative splicing; appetite
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ed. No. 4.5e-238;
Mismatches 119;
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ilarity 77.3%; Pred.
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RESULT 5
568437
Leptin receptor, splice form Ob-Ra - mouse
C; Species: Mus musculus (house mouse)
C; Accession: S68437
R; Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R; Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R; Lee, G.H.; Proenca and Splicing of the leptin receptor in diabetic mice.
A; Reference number: S68437; MUID:96231997
A; Accession: S68437
A; Accession: S68438
A; Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
A; Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
A; Cross-references: Splice form Ra; tissue hypothalamus
A; Resperimental source: splice form Ra; tissue hypothalamus
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C; Comment: For alternative splicing; appetite
C; Keywords: alternative splicing; appetite
                                                                                                        780
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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VTFSNLKATRPRGKFTYDAVYCCNEQACHH
                             SSCVIVSWILSPSDYKLMYFIIEWKNLNED
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                    RYABLYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH
                                                                                                      QIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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tissue type brain
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Mismatches 123;
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No. 2e-234;
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3-Feb-1998
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$74225
leptin receptor, isoform Ob-Rf - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-Jan-1998 #sequence_revision 13-Feb-199
C; Accession: $74225
R; Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R
FEBS Lett. 392, 87-90, 1996
A; Title: A novel leptin receptor isoform in rat.
A; Reference number: $74225; MUID:96368027
A; Accession: $74225
A; Molecule type: mRNA
A; Residues: 1-895 < WAN>
A; Experimental source: strain Sprague-Dawley; tis.
C; Genetics:
                                                                                                                                                                                                                                                                                                                A;Gene: rOb-R
C;Keywords: appetite; transmembrane prot
F;840-860/Domain: transmembrane #status
                                                                                                    SSVKAEITINIGLLKISWEKPVFPENNLOF
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ISSKQIVWWRNLAEKIPEIQYSIVSDRVSK
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nilarity 76.5%;
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C. Species: Mus musculus (house mouse)
C. Saccession: 568441
R. Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R. Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R. Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R. Title: Abnormal splicing of the leptin receptor in diabetic mice.
A; Reference number: 568437; MuID:96231997
A; Accession: 568441
A; Accession: S68441
A; Accession: S68441
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-805 < LEE>
A; Residues: Leftences: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A; Residues: Leftences: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A; Residues: Leftences: EMBL:U49110; NID:g1195493
A; Residues: Leftences: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A; Residues: Leftences: EMBL:U49110; NID:g1195493; PIR:S68438, PIR:S68438, PIR:S68439, PIR:CGenetics:
A; Repwords: alternative splicing; appetite
C; Keywords: alternative splicing; appetite
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change
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Σ	Matches 608; Conservative 73; Mismatches 115; Indels 2; Gaps 2;	A; Cross-references: GB: M83336; NID: g193591; PIDN:
o da	1 MICQKECVVLLHWEFIYVITARNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60 :	Status: transla Molecule type: Residues: 1-917
oy G	YETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADN 	A; Cross-references: EMBL:X62646; NID:9840816; PID C; Genetics: A; Gene: 9p130 C; Superfamily: cytokine receptor homology
Qy Db	1 QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS 1 :1: : : : :	Keywords: glycoprotein 134-314/Domain: cytokine receptor homo
δο O	81 FOMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 2	Query Match Best Local Similarity 20.9%; Pred. No. 1.2e-Matches 191; Conservative 140; Mismatches
cy B	41 LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 30	323
Oy Op	301 GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360 	363 SKEIVWWMNLAEK : 62 ASYIVWKTNHA-A
Oy Db	361 VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420 : :	423 AELYVIDVNINISC-ETDGYLTKMTCRW : :
Qy	421 RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480	474 SDIPSIHPISEPKDCYLQSD :: 166 TEKFPDCQSK
QY D	481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540	532 DSVVKPLPPSSVKAEITINI-GLLKIS: :: : : : 215 VDKVKPTPPYNLSVTNSEELSSILKLS
oy D	541 SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600 	583 262
O _Y	601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660	QY 636 IKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDSLC : : :: :
Qy Dp	4KNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 7 	QY 694 DVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTFS
QY	21 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 7	OY 753 CVIVSWILSPSDYKLMYFIIEWKNLNEDGEIKWLRIS : : : : : :
oy E	81 GEIKWLRISSSVKKYYIH 798 	OY 811 LYPIFMEG
RES	1	OY 819VGKPKIINSFTQDDIEKHQSDAGLY :: :
ት ድር ር ልሂ	149699 31 ycoprotein 130 - mouse 2; Species: Mus musculus (house mouse) 2; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000	Qy 844VIVPVIISSSI-LLLGTLLISHQRMKKLFWE :: ::
, R 4 	lbi, M.; Taga 1992 of a murine I	OY 895 FEHLFIKHTASVTCGPLLLEPETISEDISVDTSWKNKDE
A A A A	MUID:92291532 B/EMBL/DDBJ	951GSVCISDQFNSVNFS
A;R	esidues: 1-917 <res></res>	

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LPSVQLT-----CNILSFGQIE 112
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| SAQSTASTVEYSTVVHSGYRHQV 769
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PG----RETYLETNYTLKSEWA 165
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SIKDSGKGYWSDWSEEASGTTYE 321
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                                                                                                                                                                                                                                                                                                                                              KPRGKFTYDAVYCCNEHECHHRY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOFQIRYGLSG----- 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VSSGLGGLLDLKSDIQYRT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCSVQRY - - VINHHTSCNGTWSE 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | : : | : : NGKILDYEVILTQSKSVSQTYTV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSSVKKYYIHDHFIPIEKYQFS 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDVPNPKNCSWAQGLNFOKPET 894
                                                                                IDN:CAA44515.1; PID:9840817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | : | | | KKPCPDD----LKSVDLFKKEKV 717
                                                                                                                                                                                                            B 2; Length 917;
e-15;
338; Indels 244; Gaps
                                                                                                                                                                                                                                                                                                   QRGSNFTAICVLKEACLQHYYVN 61
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QY 999 GEEQGLINSSVTK-CFSSKNSP 	PLKDSFSNSSWEIEAQAFFILSDQHPNIISPHLTF 1053	Qy 82
1054 SEGLDELLKLEGN 1066		
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oprotein gp130 pre mo sapiens (man) r-1991 #sequence_r A36337 urakami, M.; Saito	cursor - human evision 12-Apr-1991 #text_change 28-Jul-2000 , M.; Hirano, T.; Taga, T.; Kishimoto, T.	
cular cloning and umber: A36337; MUI	expression of an IL-6 signal transducer, gp130.	4 <u>y</u> 98
iiminary pe: mRNA -918 <hib> ences: GB:M57230;</hib>	NID:g186353; PIDN:AAA59155.1; PID:g186354	RESULT A44257 interleu C;Specie
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OY 337 PPKILTSVGSNVSFHCIYKK bb 33 PESPVVQLHSNFTAVCVLKEKCM	ENKIVPSKEIVWWMNLAEKIPOSQYDVVSDHVSKVTF 393 : :	A; Note: C; Superf C; Keywor F; 134-31
Qy 394 FNLNETKPRGKFTYDAVYCCNEHECHHRYAELYVIDV :: 1	KFTYDAVYCCNEHECHHRYAELYVIDVNINISC-ETDGYLTK 444 ::	Query Best L
OY 445 MTCRWSTSTIOSLAESTLOLRYHI	MTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQP 502 	Match 3
OY 503 IFLLSGYTMWIRINHSLGSLDSP :::::: ::: : Db YFVN-IEVWVEAENALGKVTSD	SPPTCVLPDSVVKPLPPSSVKAEITINIGLLKISW 558 : SDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTW 244	m
QY 559 EKPVFPENNLQFQIRYGLSG : : : :: : Db 245 TNPSIKSVILKYNIQYRTKDAST-	GLSGKEVQWKMYEVYDAKSKSVSLPVPDLCAVYAVQV 611 :	
Oy 612 RCKRLDGLGYWSNWSNPAYTVVM 	RCKRLDGLGYWSNWSNPAYTVVWDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKND 671 	
QY 672 SLCSVQRYVINHHTSCNGTWSEDVGNH : : ! : : : : DS : : : : : : : : :	EDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANF 727 : :	
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786 LRISSSVKKYXIHDHFIPIEK		Db 27 Qy 65
DD 4/1 QQEDGIVHKIILKGNLAESKCIL	ILITYIPYIADGPGSPESIKAILKQAPPSKGPTVRTKKV 530	Dp 33

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Ye,; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.

14. 666-672, 1992

15. 14. 666-672, 1992

15. Molecular cloning and characterization of the rat liver IL-6 signal transductence number: A44257; MUID:93052397

16. Signal translation

16. Signal translation

17. Signal translation

18. Signal transduction

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29. Signal translation

20. Signal tr
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tes: Rattus norvegicus (Norway rat)
: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
sion: A44257
                                                                                                                                                                                                                                                                                 649
843
                                                                                                                                                                                                                                                                                                                                                                           70 LFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSWK 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 VFTTQDVI-----YFPPKILTSVGSNVSFHCIYKKENKIVPSKE---IVWWMNLAE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 GKNEAVLEWDOLPVDVONGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT-LYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 KIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVY-----CCNEHECHHRYAELYVI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TDVVFQNVQLTCNILSFGQIEQNVYGIT
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                                                                                                                                                                                                                                                ::||| :: | :|| | :: | || 90 VRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLFCFNKRDLIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...-NFN
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   -NSFTQDDIEKHQSDAGLY-
                                                                                                                                                                                    -VIVPVIISSSI-LLLGTLLISHQR--MKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LDLFKKEKINTEGHSSGIGGSS---CMSSSRPSISSSDENES 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 5.4%; Score 339.5; DB 2; Local Similarity 20.8%; Pred. No. 6.3e-14; es 185; Conservative 141; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RH----
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AVPKEQVTVINRTASSVTF-----
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SKDQM-----
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40;

209 150 150 323 323 529 529 586 586 586 729	Db 248 GCLMLSW-KPWKPSENHEQECELRYQPOLKGANWTLVFHLPSSKDOFELCGLHQA 301 Cy GCLMLSW-KPWKPSENHEQECELRYQPOLKGANWTLVFHLPSSKDOFELCGLHQA 301 Db 302 PVYTLQMRCIRSSLPGEWSPMS-PGLQLRPTMKRAPTINGDTMKKEK 658 :
AREALD 113 AREALD 114 AREALD 115 AREALD 115 AREALD 117 AREALD 117 AREALD 117 AREALD 117 AREALD 117 AREA 117 ARE	966EAEGTEVTYEDES 1003 GLINSSVTKCFSKNSPLKDS 1003 GLINSSVTKCFSKNSPLKDS 1057 OYIRSDSTQPLLGGPTPSPKS 1055EGLDELLKLEGNF 106

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ECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPPLGLHMEIT- : : ! : :	SNVSFHCIYKKENKIVPSKEIVWWMNLAEKIPOSQYDVVSDHVS : :	STLQ STLQ GSLD GSLD	NEQ ::: SVQ SVQ NPA NKK	CNG L: CSS CSE L: CSE			LEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVC :
195 90 249 149 295 205	346 265 403	460 460 367 520 517	567 475 627 524	687 575 742 635	796 686 833 746	840 806 868 868	913 921 970 969 1015
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A; Cross-references: GB: X55721; NID: 931696; PIDN: CAA39253.1; PID: 931697
A; Note: clone 25-1; placenta
R; Seto, Y; Fukunaga, R; Nagata, S.
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A; Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A; Reference number: A46486; MUD: 92091782
A; Reference number: A46486
A; Status: preliminary
A; Residues: B55-863 < SET>
A; Molecule type: DNA
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A; Residues: B55-863 < SETO MUD: 924, 344-356, 1995
A; Experimental source: granulocyte
A; Note: sequence extracted from NCBI backbone (NCBIN: 71484, NCBIP: 71485)
A; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys: 324, 344-356, 1995
A; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
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A; Molecule type: protein
A; Residues: 234-269 < HAN>
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A; Genes: GDB:126430; OMIM:138971
A; Map position: 1p35-1p34.3
C; Keywords: alternative splicing; glycoprotein; transmembrane protein
C; Keywords: alternative splicing; glycoprotein; transmembrane protein
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F; 25-863/Product: granulocyte colony-stimulating factor receptor, long form #status predicted <EXT>
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F; 628-653/Domain: transmembrane #status predicted <IVM>
F; 654-863/Domain: intracellular #status predicted <IVM
F; 654-863/Domain: intracellular #status predicte
granulocyte colony-stimulating factor receptor precursor, long form - human N; Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C; Accession: C38252; A38252; JH0330; A46486; S68332; S21607
C; Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R; Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
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A; Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
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A; Status: preliminary
A; Molecule type: mRNA
A; Status: preliminary
A; Molecule type: mRNA
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A; Molecule type: mRNA
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A; Note: clone pHQ3
A; Note: clone pHQ3
B; Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
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A; Title: Expression cloning of a human granulocyte colony-stimulating factor receptor A; Reference number: JH0329; MUID:91079757
A; Accession: JH0339; MUID:91079757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNĀ
A;Residues: 1-863 <FUK>
A;Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A;Ote: clones pHG11 and pHG5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 ETKPRGKFTYDAVYCCNEHECHHRYAELYVID-
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A; Status: preliminary
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:	Best Local Similarity 20,3%; Pred. No. 2e-10; Matches 153; Conservative 121; Mismatches 287; Indels 192; Gaps 35;
QY 447 CRWSTSTIQSLAES-TLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECI 499	Qy 341 LTSVGSNVSFHCIYKKE-NKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLN 397 : : :: :: :: :
Qy 500FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEIT 548 :: :	QY 398 ETKPRGKFTYDAVYCCNEHECHHRYAELYVIDVNINISCETDGYLFKMT 446 1:
Qy 549 INIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVP 601 :	Qy 447 CRWSTSTIQSLAES-TLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECI 499
Qy 602 -DLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIIN 650	QY 500FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEIT 548 : : :
OY 651 GDTMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKF 701 :	Qy 549 INIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVP 601 :: :: : Db 244 PQAGCLQLCWE-PWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQ 291
Oy 702 TFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILS 761 : : :	QY 602 -DLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIIN 650 :11: :1:11 :1:11 :1:1
Qy 762 PSDYKLMYFIIEWKNLNEDGEIKW-LRISSSVKKYYIHDHFIPIEKYQFSLYP 813 ::	QY 651 GDTMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKF 701 :
Qy 814 IFMEGVGKPKIINSFTQDDIEKHQSDAGLYVIVPVIISSSILLLGTLLI 862 ::::::::::::::::::::::::::::::::::::	Oy 702 TFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILS 761 : :
Qy 863 SHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKHTASVT 907	Qy 762 PSDYKLMYFIIEWKNLNEDGEIKW-LRISSSVKKYYHDHFIPIEKYQFSLYP 813 :: : : : : : : : Db 451 PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLKENIRPFQLYEIIVTP 506
Qy 908 CGPLLLEPETISEDISVDTSWKNKDEMMPT 937 :	QY 814 IFMEGVGKPKIINSFTQDDIEKHQSDAGLYVIVPVIISSSILLLGTLLI 862 ::::::::::::::::::::::::::::::::::::
OY 938TVVSLLSTTDLEKGSVCISDQFNSVNFSEAEGTEVTYEDESQROP 982 :: :: :: bb 674 VPTIMEELPGPRQGQWLGQTSEMSRALTPHPCVQDAFQLPGLGTPPITKLTVLEEDEKKP 733	Qy 863 SHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKHTASVT 907 : : : 564IFWTNAQNQSFSAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 613
ESULT 14 H0329	Qy 908 CGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLE 949 :
<pre>granulocyte colony-stimulating factor receptor D7 precursor - human C;Species: Homo sapiens (man) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999 C;Date: 12-Feb-1999; \$21608 C;Accession: JH0329; \$21608 R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor</pre>	Qy 950 KGSVCISDQFNSVNFSEAEGTEVTYEDESQRQP 982 ::
. Exp.] ;Title: ;Refere	SULT 15 0312
Molecu Residu Cross-	ferentia pectes: ate: 28- ccession
<pre>:Experimental source: placen :Keywords: glycoprotein; tra ;1-24/Domain: signal sequenc ;25-783/Product: granulocyte</pre>	Jomida, M.; ramamoto-ramaç Biochem. 115, 557-562, 19 Title: Three different CDN Reference number: JX0312;
;25-627/Domain: extracellular #status predicted;628-653/Domain: transmembrane #status predicted;654-783/Domain: intracellular #status predicted;93,128,134,389,474,579,610/Binding site: carboh	Accession: JX0312 Molecule type: mRl Residues: 1-1092 d Pross-references:
Query Match 4.5%; Score 284; DB 2; Length 783;	A;Accession: JC2181 A;Molecule type: mRNA A;Residues: 1-717,'EA' <tom1></tom1>

A; Cross- A; Experi R; Tomida FEBS Let	references: I mental source , M.; Yamamot t. 334, 193-1
A; Title: A; Refere A; Access A; Status	Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mous Reference number: S38942; MUID:94039833 Accession: S38942 Status: preliminary
A; Molec A; Resic A; Cross C; Keywc F; 1-43,	Molecule type: mRNA Residues: 1-717, EA' <tom2> Cross-references: GB:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494 Cross-references: GB:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494 Reywords: differentiation; receptor; transmembrane protein 1-43/Domain: signal sequence #status predicted <sig> 44-1092/Product: differentiation-stimulating factor/leukemia inhibitory factor recepto</sig></tom2>
F; 828-{ Ouer;	in: transmembrane #status predicted <tmm> 4.5%; Score 281.5; DB 2; Length 1092;</tmm>
Best Matc)	Best Local Similarity 18.8%; Fred. No. 4.9e-10; Matches 217; Conservative 177; Mismatches 392; Indels 371; Gaps 57;
, te	178 KGSFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSP- 225 : :
Oy ,	226
ζ.	266 PLQYQVKYSENSTTVIREADKIVSATSLLVDSILPGSSYEVQVRGK 311
QQ	::: : ::
	312 RLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKIVPS 363
	DIDSFRESCINEMSDWSFLANTSWIKNIEINVERQUNVVERGSNMILCC
oy oy	364 KEIVWWM-NLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHEC 418 :
0y	419 HHRYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTL 462
op QC	: : : :
	QLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINH
QQ	374 SAVFHRIEGLTNETYRLGV-QMHPGQEIHNFTLTGRN 409
Oy do	518 SLGSLDSPPTCVLPDSVVRPLPPSSVRAEITINIGLLKISWEKP-VFPENNLQFQIRYGL 576
οy	577 SGKEVQWKMYEVYDAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVM 634 : : : : : ! ! !
Dp 4	468 ANSKKEVRNATIRGAEDSTYHVAVDKLNPYTAYTFRVRCSS-KTFWKWSRWSDEKRHLTT 526
oy G	635 DIKVPMRGPEFWRIINGDIMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSED 694 : : : : : : : :
	S VGNHTKETEIMTEOAHTVTVIAINSIGASVANENITESWPMSKVNIVOS
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λo	IVSWILSPSDYK
qq	632 VGLGNRIFLTWRHDPNMTCDYVIKWCNSSRSEPCLLDWRKVPSNSTETVIE 682
op Qo	683 SDQFQPGVRYNFYLYGCTNQGYQLLRSIIGYVEELAPIVAPNFTVEDTSADSILVKWDDI 742

<u>></u>	833)	842
۾	743	PVEELRGFLRGYLFYFQKGERDTPKTRSLEPHHSDIKLKNITDISQKTLRIADLQGKTSY	802
<u>></u> ,	843		869
۵	803	803 HLVLRAYTHGGLGPEKSMFVVTKENSVGLIIAILIPVAVAVIVGVVTSILCYRKREWIKE	862
<u>></u> •	870	LFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSWK	929
Ď	863	: :	910
<u>≻</u>	930	PTDLEKGSVCISDQFNSVNFSEAEG	975
ð	911	: :: :: ::	970
≱	916	D-ESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIEAQ	1034
۾	971	: ; ; DVQSMYQPQAKAEEEQDVDVQSMYQPQAK	991
	1035	AFFILSDOHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYLGVTSIKKRESG	1091
۾	992	VVAGYKPOMRLPISPAVEDTAAEDEEGKTAGYRPQANVNTWNLVSPDSPRS	1042
≱ •	1092	1092 VLLTDKSRVSCPFPAPC 1108	
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Search completed: August 15, 2002, 16:25:01 Job time: 301 sec

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Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

sw model - protein search, using OM protein

Run on:

Search time 101.13 Seconds
(without alignments)
1279.551 Million cell updates/sec 2002, 16:18:50; August 15,

US-08-779-457-2 6254 Title:

.... QTCSTQTHKIMENKMCDLTV 1165 1 MICOKFCVVLLHWEFIYVIT. score: Sequence:

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747574 hits satisfying chosen parameters: of Total number

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Searched:

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Database

old-geneseg/genesegp-embl/AA1980.DAT:*
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predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the t

SUMMARIES

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	Description	Human WSX receptor	Human Ob receptor	Obesity receptor D	Human Ób receptor	Peptide Sed ID No:	Human Ob receptor,	Human ob-receptor	Obesity receptor C	Human WSX receptor	Human WSX receptor	Obesity receptor A
	ID	AAW24051	AAE12609	AAW34500	AAE12551	AAY13474	AAW19116	AAW62544	AAW34499	AAW24052	AAW24053	AAW34497
		18	22	18	22	20	18	19	18	18	18	1.8
	Query Match Length DB	1165	1165	1220	1165	1165	1165	1221	970	896	923	972
₩°	Query Match	100.0	100.0	100.0	6.66	99.9	8.66	92.9	77.3	77.2	77.2	77.2
	Score	6254	6254	6254	6250	6246	6240	5809	4831.5	4826	4826	4826
	Result No.	1	7 7	m	4	S	9	7	80	6	10	11

Obesity receptor B Human OB-R variant Human OB-R leptin Human OB-R leptin Human OB-R variant Human OB-R variant Haematopoietin rec Haematopoietin rec Haematopoietin rec Variant form of hu Human haemopoietin Rat wild-type ob r Rat ob receptor (# Rat ob receptor (# Rutine long form O Murine long form O Peptide Seq ID No: Human Ob-receptor Obesity receptor Obesity receptor Obesity receptor Fat ob receptor Obesity receptor Obesity receptor Obesity receptor Obesity receptor	Rat ob receptor is Ob protein recepto Rat ob receptor is Murine WSX recepto Murine short form Ob protein recepto Murine leptin rece Murine leptin rece
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ALIGNMENTS

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Human; WSX receptor; variant 13.2; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
                     AAW24051 standard; Protein; 1165 AA
                                                                                          Human WSX receptor variant 13.2
                                                                                                                                                                                                                                                                                   97WO-US00325
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96US-0585005
                                                                   (first entry)
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08-JAN-1996;
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Kim KJ, Chiang NY, Carter PJ, (GETH) GENENTECH INC. Bennett B,

Rodrigues ML:

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                                                                                                              which can be used to identify and purify ligands and activators.

An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also contains to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or contained blood cell lineages. This is useful when a mammal, caused blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to treat, construction disease, cardiovascular diseases, cardiova
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98US-0069781. 29-APR-1998;

95US-0562663 95US-0566622... 95US-0569485. 95US-0570142. 95US-0583153. 96US-0599455. 96US-0638524. 96US-0708123. 04-DEC-1995; 08-DEC-1995; 11-DEC-1995; 28-DEC-1995; 22-JAN-1996; 26-APR-1996; 03-SEP-1996; 28-MAY-1997;

(MILL-) MILLENNIUM PHARM INC

JA, Culpeppe RI, Tepper WPI; 2001-624489/72. N-PSDB; AAD20509. Tartaglia LA,

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body weight disorder, e.g. obesity, tacting cell expressing mammalian Ob mammalian SOCS-1 protein with test Identifying compounds for treating anorexia or cachexia, comprises con receptor protein, JAK2 protein and compound

Claim 1; Fig 3; 109pp; English.

nucleic acids on of mammalian sins and nuc requlation proteins the (ObR) The patent discloses obese receptor encoding them. ObR protein particip

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and anorexia
body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ObR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ObR gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexiathe present sequence is ObR protein from human.
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                                                              This sequence represents the obesity (OB) receptor D protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.
                receptor(s) and related DNA - used to treat weight obesity, diabetes and high cholesterol or blood
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Matches 1165; Conservative
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/label= Extracellule
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/note= "Asn is N-gly
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/note= "Asn is N-gly
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therapy; obesity; cachexia;
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The patent discloses obese receptor (ODR) proteins and nucleic acids encoding them. ODR protein participates in the regulation of mammalian body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ODR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ober gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia. The present sequence is human ODR protein mutant (Y1141F).
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/note="Conserved motif of cytokine I receptor family"
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/note= "Asn is N-glycosylated"
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/label- Transmembrane_domain
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95US-0566622.
95US-0569485.
95US-0583153.
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96US-0638524.
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28-DEC-1995;
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The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine-985 phosphorylated leptin receptor with tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-1D or its fragment in the presence and absence of a candidate agent under conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-1D or its fragment can be detected; and (b) detecting the binding of the phosphorylated leptin receptor and PTP 1D; where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent indicates that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin receptor-dependent PTP-1D phosphorylation are useful as drugs in weight content of animals, particularly in mammals. Disorders that can be treated by PTP-1D modulators include conscity and its associated diseases, e.g. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally the agents identified may be useful in agriculture where body weight of domestic animals can be
                                                                                                                                                                                                                                                                                                                                                                                             Leptin; phosphorylated leptin receptor; tyrosine phosphatase 1D; PTP-1D; modulator; drug; weight loss; adiposity; hypertension;, heart disease; type II diabetes; cancer; AIDS: agriculture.
agents that modulate leptin activity
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Human Ob receptor (ObR) (AAW19116) is a novel polypeptide that participates in the control of body weight and which is involved in signal transduction triggered by the binding of its natural ligand, Ob (leptin). It is a member of the class I cytokine receptor family. Its amino acid sequence was deduced from a foetal brain cDNA clone (AAT69592). The receptor corresponds to the long form mouse ObR (AAW19115). ObR proteins, peptides, antibodies, agonists and antagonists can be used in the diagnosis and treatment of body weight disorders such as obesity, cachexia and anorexia.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
SEQUENCE FROM N.A.
Song X.T., Feng Z.O., Guan X.H.;
Song X.T., Feng Z.O., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy cha variable region gene of monoclonal anti-idiotypic antibody NP3 Schistosoma japonicum.";
Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282622; AAG01452.1; -.
HSSP; P01772; ZFB4.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.W.
InterPro; IPR003596; Ig.W.
R Ffam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG.like; 1.
INON_TER 119 A1; 13567 WW; BA893873FD5FA6AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Clemens A., Rademaekers A., Specht C., Koelsch E.;

Clemens A., Rademaekers A., Specht C., Koelsch E.;

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ225174; CAB65237.1; -.

R HSSP; P01810; 2FBJ.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_v.

R Pfam; PF00047; ig; 1.

R SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119,
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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Pred. No. 1.4e-29;
13; Mismatches 20
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Best Local Similarity 67.7%;
Matches 86; Conservative 1
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     AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRY--YGSSAYHRGSYYMDVWG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Trematoda; Digenea; Strigeidida; ; Schistosoma.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ed. No. 7.2e-29;
Mismatches 28;
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Strausberg R.;
Submitted (R.;
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Submitted (R.;
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; 1MCP.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003506; Ig_AHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00400; IG_1ike; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; 0A9BF43
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Eukaryota; Metazoa; Platyhelminthes
Schistosomatoidea; Schistosomatidae
NCBI_TaxID=6182;
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Pred.
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6
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69.0%;
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226 VVCKVQHPNGN 236
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Best Local Similarity
Matches 89; Conserv
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KGTTVTVSS 147
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DDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-C57BL/6;

Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Rydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067781; BAB63266.1; -.

NON_TER 1 1

NON_TER 1 46

SEQUENCE 146 AA; 16216 MW; 92460FIFDFIB7538 CRC64;
                                                                                                                                                                                  0924R8
0924R8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WH186.2-D-J-C MU PROTEIN (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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EDSAVYYCARDRYYA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKGKATLTVDKSSSTAYMQLNSLTSI
61 AOKFOGRVTMTRDTSIGTAYMELSRLSSI
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                                                                  121 TLVTVSS 127
                                                                                                   111 TSVTVSS 117
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| 115 TTLTVSS 121
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0924R8
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                                           Length 145;
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                  55A59A7908B2CD6A CRC64;
                                          ; Score 429.5; DB 11;
; Pred. No. 8.5e-28;
19; Mismatches 21;
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1
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16141 MW;
                                            Query Match
Best Local Similarity 63.0%;
Matches 80; Conservative 19
1
145
145 AA;
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|TTLTVSS 120
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SEQUENCE
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

August 15, 2002, 16:36:09; Run on:

Search time 28.14 Seconds (without alignments) 342.614 Million cell updates/sec

.....SRDSSGNHVVFGGGTKLTVL 249 US-08-779-457-48 1329 1 EVQLVQSGAEVKKPGASVKV... Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224 Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the t

	scription	P01714 homo sapien	вз ношо	homo	13 homo	mus m	P01751 mus musculu	P01756 mus musculu	PO1747 mus musculu	P01746 mus musculu	P06329 mus musculu	P06330 mus musculu	P01755 mus musculu	PO1745 mus musculu	P03980 mus musculu	mus	P80748 homo sapien	homo	mus m	homo	mus m	homod	homo	homo	mus ก	P01750 mus musculu	homod	homo	mus n	homod	P01754 mus musculu	P01758 mus musculu	P01808 mus musculu	P01807 mus musculu
SUMMARIES	ID	LV3A_HUMAN	HV1G_HUMAN	HV1C_HUMAN	HV1B_HUMAN	HV13_MOUSE	HV07_MOUSE	HV12_MOUSE	HV03_MOUSE	HV02_MOUSE	HV50_MOUSE	HV51_MOUSE	HV11_MOUSE	HV01_MOUSE	HV48_MOUSE	HV00_MOUSE	LV3B_HUMAN	HV1A_HUMAN	HV09_MOUSE	LV4C_HUMAN	HV04_MOUSE	LV5A_HUMAN	LV4A_HUMAN	HV1H_HUMAN	HV15_MOUSE	HV06_MOUSE	LV4B_HUMAN	LV4E_HUMAN	HV49_MOUSE	HV1F_HUMAN	HV10_MOUSE	HV14_MOUSE	HV38_MOUSE	HV37_MOUSE
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ф	Query Match				33.3	•	•			30.9	•		•	•		28.6	•		•			•	•	•	•	•	•			•	•		•	
	Score	1	483	479.5	443	434	429.5	420	415	411	410.5	403.5	395.5	385		380.5	377	376	368	366	366	364	363	361.5	361	360	358	356	355	353	352	352	349.5	4
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RESULT 2
HVIG_HUMAN

ID HVIG_HUMAN STANDARD; PRT; 117 AA.

AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1999 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;

P06327 mus musculu P01810 mus musculu P01718 homo sapien P01709 homo sapien P01760 homo sapien P06316 homo sapien P01711 homo sapien P01761 homo sapien P01761 homo sapien P01710 homo sapien P01710 homo sapien		te) date) Vertebrata; Euteleostomi; ; Hominidae; Homo.	; ce-Jones protein. 3. The of the disulfide EIN.	CRC64;	tch 39.2%; Score 521; DB 1; Length 108; al Similarity 92.5%; Pred. No. 2e-32; 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0; SELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF 202
HV52_MOUSE HV40_MOUSE LV4D_HUMAN LV2F_HUMAN HV05_MOUSE HV1D_HUMAN LV1G_HUMAN LV2H_HUMAN HV3G_HUMAN LV2K_HUMAN LV2K_HUMAN	ALIGNMENTS PRT; 108 AA.	d) equence update nnotation upda SH. ; Craniata; Ve ; Catarrhini;	Putnam F.W. bda type Ben the location).	nce-Jones protein. W; E7E1229586411A	tch 39.2%; Score 521; DB 1; Leng al Similarity 92.5%; Pred. No. 2e-32; 99; Conservative 5; Mismatches 3; In. SELTODPAVSVALGOTVRITCQGDSLRSYYASWYQQKPGQAPVLVIY
26.2 25.0 25.0 25.3 119 25.3 111 25.3 117 125.3 117 124 124.7 24.7 122 124 122 124 122 124 122 124 122 124 122 124 122 124 122 124 125 127 127 127 127 127 127 127 127 127 127	STANDARD;	86 (Rel. 01, Created 86 (Rel. 01, Last see 99 (Rel. 38, Last an Chain V-III region ens (Human). Metazoa; Chordata; Eutheria; Primates;	QUENCE. DLINE=70166723; PubMed=4909564; tani K., Wikler M., Shinoda T., he amino acid sequence of a lam mplete amino acid sequence and idges."; Biol. Chem. 245:2171-2176(1970 - MISCELLANEOUS: THIS IS A BENC R; A01980; L3HUSH. SP; P01703; 7FAB. terPro; IPR003006; Ig_MHC. terPro; IPR003596; Ig_V.	7, 19, 1. 06; IGV; 1. 1n V region; 21 86 108 108 08 AA; 11392	Similarity 39.2% Similarity 92.5% 9; Conservative TQDPAVSVALGQTVRITCY TQDPAVSVALGQTVRITCY SSGNTASLTITGAQAEDE
34 35 36 36 37 38 38 336 39 334 40 334 41 327 5 43 327 5 45 325	5 ≼'	PUL/14; 21-JUL-1986 21-JUL-1999 15-JUL-1999 19 lambda ch HOMO Sapiens Eukaryota; M Mammalia; Eu NCBI_TaxID=9;	SEQUENCE. MEDLINE=70166723; Titani K., Wikler "The amino acid secomplete amino acid bridges."; J. Biol. Chem. 245 -!- MISCELLANEOUS: PIR; A01980; L3HUS HSSP; P01703; 7FAB InterPro; IPR00309	TER JENCE	Query Match Best Local Sim Best Local Sim Matches 99; 143 SELTQDI 111111111111111111111111111111111111
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21-JUL-1986
                                                                                                                                                                                                                 Query Match
Best Local Sim:
Matches 89;
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                                                                                                                                                              CONFLICT
NON_TER
SEQUENCE
                                                                                                      MOD_RES
DISULFID
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HV1B_HUMAN
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     concepts and developments, pp.1-36
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   TGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.:
Marcel Dekker, New York (1978).
-1. MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the human cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                           to T., Kodaira M., Zong S.Q.,
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                                                                                                                                              AVY CHAIN V-1 REGION V35
    Homo
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                                                                                                                                                                                                                                                                                                                                     1CE63F8CE97BD CRC64;
    rrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lata; Vertebrata; E
rrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 heavy chain V-I region ND precursor (Fragments)
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                      e 483; DB 1; Lo. No. 1.4e-29; ismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                            MEDLINE-88296408; Pubmed-2841108; Matsuda F., Lee K.H., Nakai S., Sa Ohno H., Fukuhara S., Honjo T.; "Dispersed localization of D segments
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X07448; -; NOT_ANNOTATED_CDS
PIR; S00476; HVHU35.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                      BE6
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                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                             2;
Mammalla; Eutheria; Primates;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                     13009 MW;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.9%;
Matches 91, Conservative
                                                                                           heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
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117
117
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                                                                                                                                                                                                                                                                                                                                   117 AA;
                                   SEQUENCE FROM N.A.
MEDLINE-88296408;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
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P01744;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRG-SYYMDVWGR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-83144028; PubMed-6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                    IG HEAVY CHAIN V-I REGION ND PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                     948F9F72A5366C20 CRC64;
                                                                                                                                                                                                              T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                              Score 479.5; DB 1;
Pred. No. 3.3e-29;
16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene subgroups.";
. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-I region HG3 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
CHAIN 20 117 IG
                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                     16491 MW;
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                36.1%;
Similarity 69.5%;
39; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02024; HVHUHG.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                       InterPro; IPR003590; 19...
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; S
SIGNAL 1 19
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115
21
54
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125
147
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20
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53
125
147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Schilling J., Clevinger B., Davie J.M., Hood L.;

A schilling J., Clevinger B., Davie J.M., Hood L.;

Trearrangements in heavy chain V-region gene segments.";

L Nature 283:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

PIR; A26242; MHMSJ5.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 1.

R SMART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

DISULFID 22 96 BY SIMILARITY.

O SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||:||: |: ||: ||:|| |||:|| ||:|| DYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 HYBRIDOMA PROTEINS THAT ALSO HOWN AT 1-7 POSITIONS, MANY OF
                                                                                                                                                                        HV13_MOUSE STANDARD; PRT; 117 AA.
P01757;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Cast annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 01, Last sequence update)
16-JUL-1986 (Rel. 01, Last sequence update)
16-JUL-1986 (Rel. 01, Last sequence update)
17-JUL-1986 (Rel. 01, Last sequence update)
18-JUL-1986 (Rel.
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                                                                                                                                                     1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
                                                                           Length 117;
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                   2D3F92FC60CD1FE7 CRC64;
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18;
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                                                                           ; DB 1;
1.3e-26;
                                                                                                                                                                                                                             AQKEQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCAR 98
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No. 6.1e-26,
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17; Mismatches
                                                                                               Pred. No. 1.36
5; Mismatches
                                                                          443;
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                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.7%; Score Best Local Similarity 64.6%; Pred. Matches 82; Conservative 17; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80078170; PubMed=6765983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
HV07_MOUSE
ID HV07_MOUSE STANDARD; 1
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
 117
12946 MW;
                                                                          33.3%;
llarity 84.7%;
Conservative
117
117 AA;
                                                              Query Match
Best Local Similarity
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                          "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).

-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                                      викагуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCSI_TaxID*10090;
                                                                                                                                                                                         STRAIN-C57BL/6;
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION B1-8/186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-2,
COMPLEMENTARITY-DETERMINING-2.
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Pred. No. 1.6e-25;
9; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verte
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D SEGMENT.
JH2 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003590; 13-.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19 IG HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02034; MHMS18.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%;
ilarity 63.0%;
Conservative 1
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54
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85
117
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133 TTLTVSS 139
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                                                                                                                                                                                                                                                             Baltimore D.;
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P01756;
21-JUL-1986
21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
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NON_TER
SEQUENCE
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Best Local
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Query Match
Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            115 TLTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                      122 LVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
HV02_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | | | | | | -- DWYFDVWGAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production: the dominant anti-arsonate
n A mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-83131846; PubMed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Fur. J. Immunol. 12:1023-1032(1982).
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      data; Vertebrata; Euteleostomi;
rognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                      mouse mu chain: homology among
                                                                                                                                                                Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                                                   THE LIGHT CHAIN OF
                                                                                                                                       MEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J.,
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6.7e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDY-
                                                                                                                                                                                                                                                                                 PROTEIN HAS ALSO BEEN DETERMINED.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 36-65.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 6.76
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420;
                                                                                                                                                                                                                      heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 63.0%; Pred.
                                                                                                                                                                                                         acid sequence of
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 1g; 1.

SMART; SM00406; 1Gv; 1.

Immunoglobulin V region; Glycopy DISULFID 22 96 BY CARBOHYD 55 55 N-1 NON_TER 117 117 SEQUENCE 117 AA; 12983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
region MOPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG_MHC.
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InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_V.
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PIR; A02028; HVMSG7.
HSSP; P01789; 1MCP.
InterPro; IPR003006; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 80; Conser
 heavy chain V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
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P01747;
                                                                                                                                                                                 L.E.;
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                                                                                                                         SEQUENCE
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This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                        2 VOLVOSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGOGLEWMGWINPNSGGTNYA 61
                                                                                                                                                                                                                                                                                                                                                    Gaps
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PIR; A02028; HVMSG7.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYXG-----GSYYFDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        QKFQGRVTMTRDTS1GTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRGT
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STRAIN-A/J;
MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 411; DB 1; Length 140; larity 60.6%; Pred. No. 3.8e-24; Conservative 20; Mismatches 24; Indels
                                                                                                                                                                                                      31.2%; Score 415; DB 1; Length 120; 61.1%; Pred. No. 1.6e-24;
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
NON_TER 120 120
SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                    ed. No. 1.66
Mismatches
                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                    Best_Local Similarity 61.1
Matches 77; Conservative
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EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43. InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 79; Conser
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P01755;
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HV11_MOUSE
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    Beyreuther K., Rajewsky K.;
    expressed at high frequency in B
set of antibody structural genes."

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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                     AVYYCARDRYYGSSAYHRGSYYMDVWGRG
                                  -----GSYDFDYWGOG
 SYGINWVKQRPGQGLEWIGYINPGNGYINY
                                                                                                                                                                                                              uta, Vertebrata; Euteleostomi;
ognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                SAVYFCARSHYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 410.5; DB ]
Pred. No. 3.5e-24;
18; Mismatches 26
                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 15.3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalla; Eutheria; Rodentia; Sciurognathi; M
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"A V region determinant (idiotope) expl
lymphocytes is encoded by a large set of
EMBO J. 3:517-523(1984).
PIR; A02037; MHMS15.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
DOMAIN 106 120 J SEGMENT
DOMAIN 106 120
J SEGMENT
DISULFID 22 96 BY SIMILAR
NON_TER 120 120
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                     61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDD1
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                               EVOLOQSGAELVRAGSSVKMSCKASGYTFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.9%; Score Best Local Similarity 59.8%; Pred. Matches 76; Conservative 18; Mis
                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        13311
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                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AA;
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TTVTVSS 120
                                                                                134 TPLTVSS 140
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                                                              TLVTVSS 127
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P06329;
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P06330;
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SEQUENCE
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                                                                                                                 RESULT 10
HV50_MOUSE
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HV51_MOUSE
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PEQUENCE.

WEQUENCE.

WEDGINE-84182519; PubMed-6201362;

A Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

WI "A V region determinant (idiotope) expressed at high frequency in B

WI lymphocytes is encoded by a large set of antibody structural genes.";

BI EMBO J. 3:517-523(1984).

BR. PIR; A02040; MHMX38.

DR PIR; A02040; MHMX38.

InterPro; IPR00306; Ig_MHC.

DR InterPro; IPR003596; Ig_W.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

KW Immunoglobulin V region.

FT DOMAIN 1998 V SEGMENT.

FT DOMAIN 105 118 J SEGMENT.

FT DOMAIN 105 118 BY SIMILARITY.

FT DOMAIN 118 118

SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
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-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARG--YGYDPF-----DVWGTG 111
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region $43 precursor.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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HV48_MOUSE
P03980;
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HV00_MOUSE
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HV48_MOUSE
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Nucleic Acids Res. 8:4839-4840(1980).

Nucleic Acids Res. 8:4839-4840(1980).

PROM A MYELOMA THAT SECRETES IGG2B.

FROM A WYELOMA THAT SECRETES IGG2B.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

From A MYELOMA THAT SECRETES IGG2B.

InterPro; IPR003596; Ig_v.

From Pro0047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region.

NON_TER 121 121
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----YRLGRYF-DYWGQG 130
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                                                                                                                                                                                                                                                                                                             20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region MPC 11.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-81053741; Pubmed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                                           Length 137;
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                                                                                                                   COMPLEMENTARITY - DETERMINING - 2.
FRAMEWORK - 3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
                                                                   IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1
FRAMEWORK-2.
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ed. No. 5.2e-23;
Mismatches 25;
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2.7e-22;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA
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No. 2
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Best Local Similarity 55.9%; Pred.
Matches 71; Conservative 21; Mis
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                                            Signal
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13135 MW;
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59.8%;
InterPro; IPR003596; Ig_v. Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Sicremann 20 137
DOMAIN 20 137
DOMAIN 50 54
DOMAIN 55 68
DOMAIN 69 85
DOMAIN 86 117
DOMAIN 118 122
DOMAIN 123 137
DISULFID 41 115
NON_TER 137 AA; 15200 M
                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
∵~+~hes 76; Conserva
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TTLTVSS
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P01745;
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SEQUENCE
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HV01_MOUSE
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61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCAR-DRYYGSSAYHRGSYYMDVWGR 119
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                                                                         EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
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23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-3.

FRAMEWORK-4.
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MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilliam A.C., C.C., Tucker P.W.;

Tucker P.W.;

"Illegitimate recombination generates a class switch from delta in an igD-secreting plasmacytoma.";

Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).

Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).

R Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).

R PIR; A02033; HVMST7.

R InterPro; IPR003596; ig_W.

R Pfam; PF00047; ig; 1.

R SMART; SM00406; iGv; 1.

R SMART; SM00406; iGv; 1.

T SIGNAL 1 20

IG HEAVY CHAIN V REGION TEI

T CHAIN 21 138 IG HEAVY CHAIN V REGION TEI
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                                                                                                                                                                                                                                                                                             138 AA.
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                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                              STANDARD;
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85
117
1127
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138
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86
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128
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|TTLTVSS 121
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STRAIN=A/J;
MEDLINE-79195438; PubMed=109536;
Capra J.D., Nisonoff A.;
"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from A/J mice bearing a cross-reactive idiotype.";
J. Immunol. 123:279-284(1979).
-1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION SEQUENCE.
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
21-JUL-1986 (Rel. 01, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin
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ed. No. 5.5e-22;
Mismatches 23; Indels 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02022; GIMSAA.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody.
NON_TER 114 114
  114 AA.
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    PRT;
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12555 MW;
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STANDARD;
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Best Local Similarity
Matches 77; Conserv
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SEQUENCE
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Search completed: August 15, 2002, 16:36:09
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AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120

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TLV

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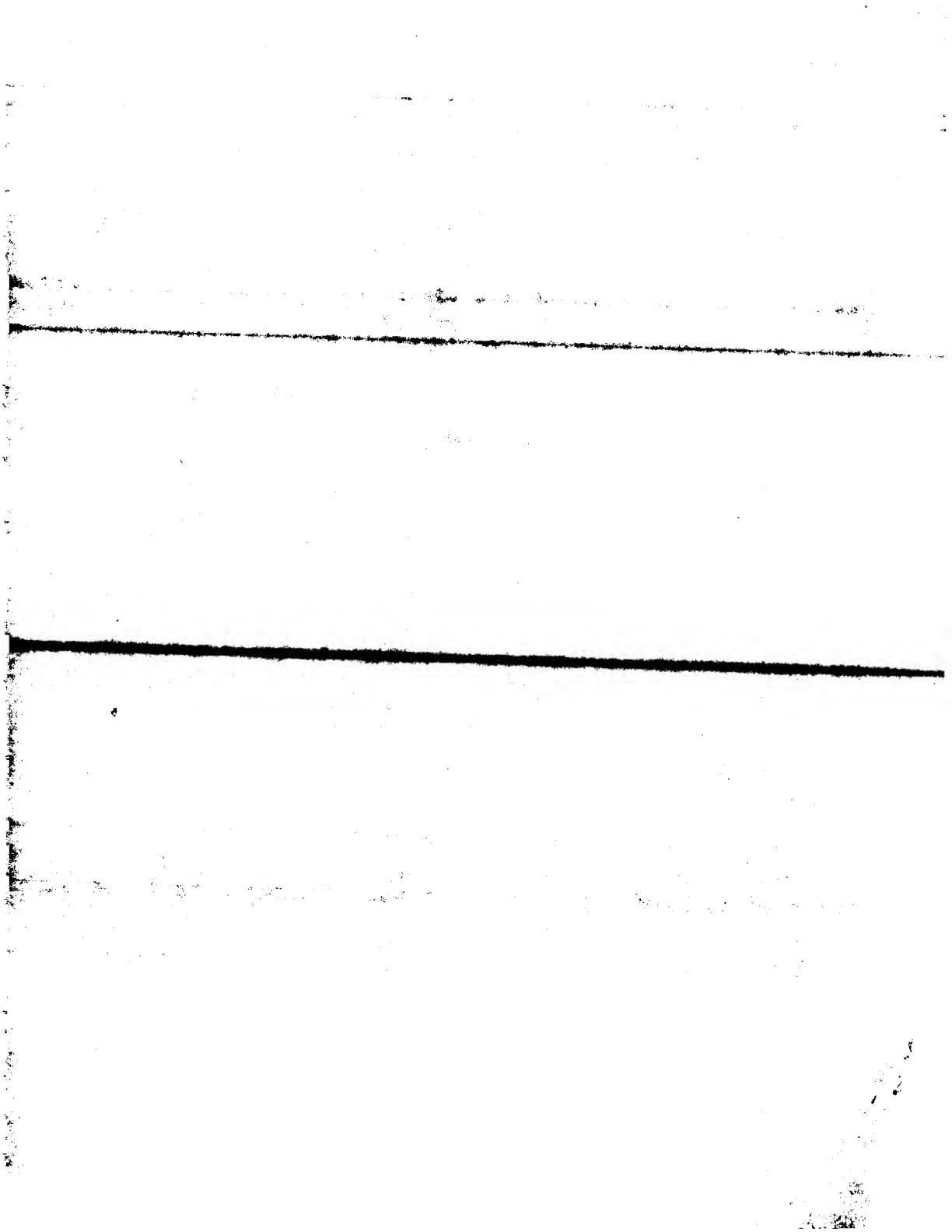
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TLV 114

112



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Thu 15 15 16:35:14 2002
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4.5 Compugen Ltd. GenCore version Copyright (c) 1993 - 2000

OM protein - protein search, using sw model

August 15, 2002, 16:25:01 Run on:

Search time 54.95 Seconds (without alignments) 435.418 Million cell updates/sec ••

....SRDSSGNHVVFGGGTKLTVL 249 1 EVQLVQSGAEVKKPGASVKV. US-08-779-457-48 1329 Perfect score: Sequence: Title:

Scoring table:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

	Description	Ig heavy chain V r		Ig heavy chain V r	3 spec	lambda chai	Ig lambda chain V	Ig heavy chain V-1		·	_	lambda chain	lambda	Ig lambda chain -	Ig heavy chain V r	lambda	Iq lambda chain V-	Ig lambda chain V-	lambda	heavy	heavy	heavy	lambda	lambda	Ig lambda chain -	heavy	heavy	heavy chain V		Ig heavy chain V r
SUMMARIES	ID	A56446	S41374	546393	JC5322	S47184	S19663	D33548	S36265	849530	S70444	S36272	S38498	S38496	S23623	S25748	ТЗНОЅН	S02083	S19672	S26938	PH1668	S18551	S36060	S13726	S25741	S26912	S31680	A32483	PH1669	36
	DB	7	(1)	7	7	~	7	~	~	7	7	7	~	N	7	7	٦	Ŋ	7	~	7	7	2	7	~	N	7	~	~	~
	Length	268	249	129	233	108	109	123	118	135	127	110	1.08	109	171	233	108	146	110	86	109	117	96	115	233	86	117	142	110	129
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S31600	869899	I44151	S34014	HVHU35	S19665	EIHUND	S31999	S31596	S26792	PL0105	S20783	PH0955	S36271	PH0960	PH1666	
N	7	7	7	↔	7	, -1	C)	~	7	N	~	N	2	a	64	
136	104	126	127	117	124	143	120	132	131	160	121	127	122	136	118	
37.0	36.8	36.7	36.6	36.3	36.1	36.1	35.3	35.1	35.0	34.9	34.7	34.7	34.5	34.5	34.4	
491.5	489	488	486	483	479.5	479.5	468.5	466.5	465	464	461	461	459	458.5	457.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug C; Accession: A56446 R; Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A. J. Biol. Chem. 270, 7829-7835, 1995 A; Title: A high affinity digoxin-binding protein displayed on M13 is: A; Reference number: A56446; MUID:95229583 A; Reference number: A56446 A; Reference type: mRNA A; Residues: 1-268 <tan> A; Cross-references: GB:U20617</tan>

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19-1996

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Gaps 9 62 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY Length 268 Indels 64; Query Match 47.8%; Score 635; DB 2; Best Local Similarity 51.6%; Pred. No. 4.7e-38; Matches 131; Conservative 37; Mismatches 64 || |||| : 229 --PETFGSGTKLEI 240 GNHVVFGGGTKLTV 248 235

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S41374
single chain Fv antibody - mouse
Single chain Fv antibody - mouse
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C; Accession: S41374
R; Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A; Description: Construction and functional characterization of a single chain Fv anti

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                                                                                                                 Length
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d. No. 4.7e-36;
Mismatches 9;
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C; Species: Homo saplens (man)
C; Accession: $46393
R; Figini, M.; Marks, J.D.; Winter, G.; Gr.J.; Mol. Biol. 239, 68-78, 1994
A; Title: In vitro assembly of repertoires A; Reference number: $46390; MUD:94254092
A; Accession: $46393
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-129 <FIG>A; Residues: 1-129 <FIG>A; Residues: I-129 <FIG>A; Residues: I-129 <FIG>A; Residues: immunoglobulin V region: i C; Keywords: heterotetramer; immunoglobulin F; 15-98/Domain: immunoglobulin homology <
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Pred.
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Pred.
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p53 specific single-chain antibody Pab/
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ilarity 51.2%;
Conservative 3
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Best Local Similarity 87.6%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    229 NSRDSSGNHVVFGGGTKL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                243
A; Reference number: S41374
A; Accession: S41374
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-249 <ART>
A; Cross-references: EMBL: Z29480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain V region - human
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Matches 132; Conser
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RESULT 5
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Ig lambda chain - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C; Accession: $47184
R; McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A; Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from pat
A; Reference number: $47181
A; Reference number: $47184
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-108 <MCI>A; Cross-references: EMBL: X79783; NID: 9506426; PIDN: CAA56179.1; PID: 9506427
C; Superfamily: immunoglobulin V region: immunoglobulin
C; Keywords: heterofetramer; immunoglobulin
F; 15-89/Domain: immunoglobulin homology <IMM>
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                     #text_change 18-Jul-1997
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                                                                                                                                                                                                                                                                                                                                                                                            61
C; Species: Homo sapiens (man)
C; Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1:
C; Accession: JC5322
R; Jacoby. C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A; Title: Characterization of scFv-421, a single-chain antibody targeted A; Reference number: JC5322; MUID:97168950
A; Reference number: JC5322; MUID:97168950
A; Reference number: JC5322
A; Molecule type: mRNA
A; Residues: 1-233 < JAN>
A; Residues: 1-233 < JAN>
C; Comment: This protein specifically binds the tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRGTLVTV
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PGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHIRELTRSE-
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0
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Pred. No. 2.7e-33;
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100.0%; Pre
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22; Conservative
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RESULT

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high specificity from phage display librarie
       M.J.; McCafferty,
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C; Species: Homo saplens (man)
C; Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C; Accession: $49530
C; Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A; Description: Molecular characterization of natural human anti-Sm autoantibodies.
A; Reference number: $48797
A; Accession: $49530
A; Accession: $49530
A; Accession: $49530
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-135 < MAH>
A; Residues: 1-135 < MAH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage displa; Reference number: S36256; MUID: 93178448
A;Reference number: S36255
A;Recession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>A;Cross-references: EMBL: Z18846; NID: 933121; PIDN: CAA79298.1; PID: 9939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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|--YLDYWGOG
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C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
C; Accession: S70444; S70426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 546.5; DB 2;
Pred. No. 4.2e-32;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                        Score 547.5; DB 2;
Pred. No. 3.1e-32;
5; Mismatches 8;

    human (fragment)

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                                                                                                                                                                                                                                                                                                                        41.2%;
illarity 81.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
41.1%;
Best Local Similarity 83.5%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     104;
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S70444
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                                                                                                                                                                antibodies from V-gene libraries displayed
                                                                                                                       A.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igheavy chain V-1 region (WIL2) - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C; Accession: D33548
R; Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A; Title: Developmentally restricted immunoglobulin heavy chain variable region A; Reference number: A33548; MUID:89345575
A; Reference number: A33548
A; Reference number: A33548
A; Reference number: A33548
A; Reference number: A33548
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>
C; Keywords: heterotetramer; immunoglobulin
E; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C; Accession: S36265
                                                                         20-Jun-2000
                                                                                                                    Griffiths,
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                                                                                                                                                                                                                                                                            NID:g29492; PIDN:CAA43821.1; PID:g1340166 region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR 201
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                                                                        22-Jan-1993 #text_change
                                                                                                                    Bonnert, T.P.; McCafferty, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVL 249
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Pred. No. 3.6e-33;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                ore 562; DB 2; 1
red. No. 2.7e-33;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 22-Jan-1993 #sequence_revision 22-Ja
C; Accession: S19663
R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.J. Mol. Biol. 222, 581-597, 1991
A; Title: By-passing immunization. Human antifa, A; Reference number: S19663; MUID: 92085276
A; Mccession: S19663
A; Molecule type: mRNA
                             Ig lambda chain V region (clone alpha-BSA3)
                                                                                                                                                                                                                                                A; Residues: 1-109 <AR>
A; Residues: 1-109 <AR>
Cross-references: EMBL:X61640; NID:g29497
C; Superfamily: immunoglobulin V region; imm
C; Keywords: heterotetramer; immunoglobulin
F; 15-89/Domain: immunoglobulin homology <IN
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illarity 82,7%;
Conservative
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Best Local Similarity
Matches 105; Conserv
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Best Local S
Matches 108
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Length 108;

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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; T submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens A;Reference number: S38498
A;Reference number: S38498
A;Accession: S38498
A;Accession: S38498
A;Accession: S38498
A;Accession: S38498
A;Cross-references: EMBL:223035; NID:g414043; PIDN:CAA80570.1; PID:g414044
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;14-88/Domain: immunoglobulin homology <IMM>
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No. 2.2e-31;
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Pred.
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illarity 93.5%;
Conservative 4
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llarity 97.2%;
Conservative
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Best Local Simi
Matches 104;
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Best Local S
Matches 101
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                                               an early step of differentiation of
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R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of A;Reference number: $70442; MUID: 93024508
A;Recession: $70444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <CUI>
A;Experimental source: clone E29.1
B;Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A;Reference number: $70426
A;Accession: $70426
A;Accession: $70426
A;Accession: S70426
A;Accession: STOWAS
A;Residues: 1-90 <TON
A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-127/Product: Ig lambda chain V region (fragment) #status predi
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    human (fragment)

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$36272

Ig lambda chain V region (clone alpha-THY-29) - human (fra C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_c C; Accession: $36272
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; EMBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity A; Reference number: $36256; MUID: 93178448
A; Reference number: $36256; MUID: 93178448
A; Reference number: $36256; MUID: 93178448
A; Residues: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA
A; Residues: 1-110 <GRI>A; Cross-references: EMBL: 218833; NID: 933419; PIDN: CAA79285
C; Superfamily: immunoglobulin V region; immunoglobulin hom C; Reywords: heterotetramer; immunoglobulin F; 15-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th high specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                546; DB 2; Le
No. 4.3e-32;
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1. No. 4e-32;
4ismatches
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Pred.
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Pred.
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98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%;
ilarity 97.2%;
Conservative
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Matches 105; Conserv
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Ig heavy chain V region precursor - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: $23623
R; Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A J. Exp. Med. 175, 831-842, 1992
A; Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro A; Reference number: $23623; MUID: 92156804
C; Species: Homo sapleans (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C; Accession: 838496
R; Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe submitted to the EMBL Data Library, June 1993
A; Description: Human antibody fragments specific for human blood group antigens from A; Reference number: 838488
A; Reference number: 838488
A; Reference number: 838488
A; Reference number: 838488
A; Reference number: BMBL: 23031; NID: 9414039; PIDN: CAA80566.1; PID: 9414040
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E; 15-89/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.1e-31;
!; Mismatches 3;
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la) gene segments of the human immunoglobulin lam
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$25748
Ig lambda chain - human
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Accession: $25748
R; Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A; Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunog A; Reference number: $16439; MUID:91257162
A; Recession: $25748
A; Recession: $25748
A; Residues: 1-233 <COM>
A; Residues: 1-233 <COM>
A; Residues: 1-233 <COM>
A; Residues: 1-233 <COM>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 148-216/Domain: immunoglobulin homology <C; Keywords: heterotetramer; immunoglobulin
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-171 < OLE>
A; Cross-references: EMBL: X59702; NID: 932010; PIDN: CAA42223.1; PID: 932011
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < IMM>
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red. No. 6.8e-31;
Mismatches 24
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Best Local Similarity 68.8%; Pred.
Matches 106; Conservative 12; Mis
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Matches 99
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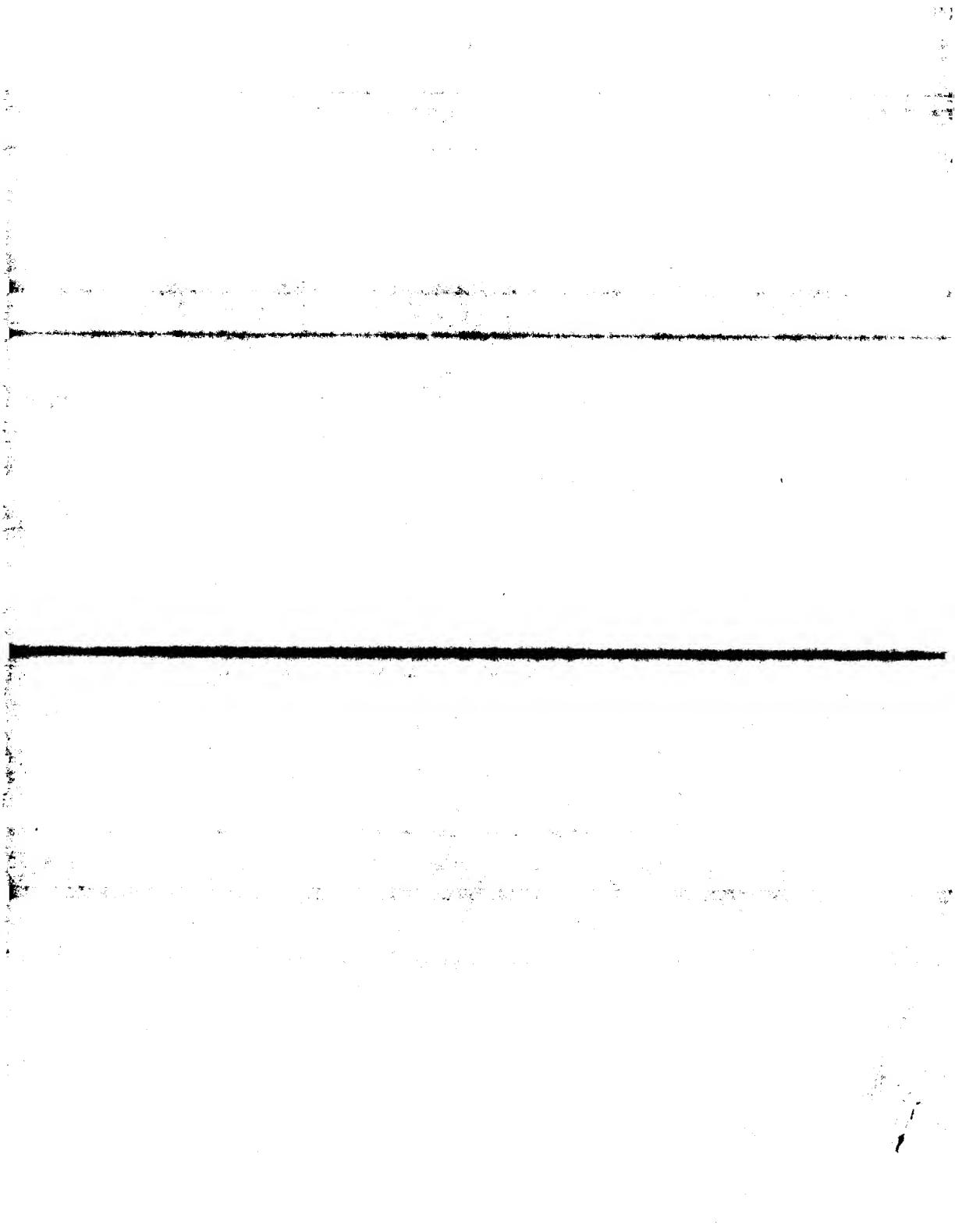
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Sequence 4, Appli
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Sequence 2, Appli
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US-08-583-153A-4
US-08-585-005-2
US-08-638-524B-4
US-08-667-197-2
US-08-708-123D-4
US-08-779-457-2
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Maximum Match 100%
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ALIGNMENTS

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RESULT 1

US-08-570-142D-4

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Sequence 4, Application US/08570142D

SEQUENCE 4, Application US/08570142D

SEQUENCE 4, Application US/08570142D

SEQUENCE 5 TOTATAGILA 1.

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tarper, Nober 1.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

TITLE OF INVENTION: OBBSITY AND CACHEXIA

NUMBER OF SEQUENCES:

ADDRESSE: Rish & Richardson, P.C.

STATE: MA

COUNTRY: Boston

STATE: MA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BM COMPATIBLE

COMPUTER: BM COMPATIBLE

COMPUTER: BM COMPATIBLE

COMPUTER: TBM COMPATIBLE

CONFICATION NUMBER: US/08/570,142D

FILING DATE: 11-DEC-1995

PRICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622
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FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
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100.0%; Pred.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
                                                        TELEPHONE: 617-542-507
TELERAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                         , ropoLOGY: unknown; MOLECULE TYPE: protein; FRAGMENT TYPE: internal US-08-570-142D-4
                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 1165; Conser
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US-08-583-153A-4

Sequence 4, Application US/08583153A

Sequence 4, Application US/08583153A

Sequence 1, Application US/08583153A

Sequence 1, Application US/08583153A

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS AND AFRATMENT OF BODY WEIG TITLE OF INVENTION: DIAGNOSIS AND AFRATMENT OF BODY WEIG TITLE OF INVENTION: OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 41

COMPRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Moston

STATE: MA

COMPUTRY: US

COMPUTRY: US

COMPUTRY: US

SOFTAND DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/583,153A

FILING DATE: US-01995

APPLICATION NUMBER: 08/56,485

FILING DATE: US-0995

APPLICATION NUMBER: 08/56,622

FILING DATE: US-0995

APPLICATION NUMBER: 08/56,622

FILING DATE: US-0995

APPLICATION NUMBER: 08/56,623

FILING DATE: US-0995

APPLICATION NUMBER: 08/56,633

FELENCHMENTARY NUMBER: 08/56,633

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches
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TELERA: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
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                                            ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-583-153A-4
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Mismatches
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Pred. No. 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flopp
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,005
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELETAX: 415/952-9881
TELETAX: 415/952-9881
TELETAX: 415/952-9881
TELETAX: 1165 amino acids
COMPUTER FORMSTICS:
LENGTH: 1165 amino acids
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GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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LOGY: Linear
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APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,524B
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 27-NOV-1995
ATORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/018001
TELECOMMUNICATION INFORMATION:
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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                                                                                                                                 Sequence 4, Application US/08638524B GENERAL INFORMATION:
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1141 YMPOFOTCSTOTHKIMENKMCDLTV
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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Matches 1165; Conser
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 NLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy discomputible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0996P1
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELES: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6254;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                        LIGANDS
                                                                    STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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100.0%; Pr/
0;
US-08-667-197-2; Sequence 2, Application US/08667197; GENERAL INFORMATION:
                                      APPLICANT: Matthews, William TITLE OF INVENTION: USES FOR NUMBER OF SEQUENCES; 47
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Matches 1165; Conservative
                                                                  NUMBER OF SEQUENCES; CORRESPONDENCE ADDRESS
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5Y: Linear
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US-08-667-197-2
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GENERAL INFORMATION:
    APPLICANT: Tartaglia, Louis A.
    APPLICANT: Tepper, Robert I.
    APPLICANT: White, David W.
    TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
    TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEITTILE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
    NUMBER OF SEQUENCES: 50
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson, P.C.
    STREET: 225 Franklin Street
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ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OOPERATING SYSTEM: Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/534
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/59,455
FILING DATE: 23-DEC-1995
APPLICATION NUMBER: 08/59,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,633
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,633
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,633
FILING DATE: 07-NOV-1995
APPLICATION NUMBER: 35,283
FILING DATE: 7-NOV-1995
ATTORNEY-AGENT INFORMATION:
TELEFAX: 200154
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 6254;
Larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-708-123D-4
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Best Local Similarity
Matches 1165; Conserv
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                       GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
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US-08-779-457-2

Sequence 2, Application US/08779457

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Chiang, Nancy Y.

APPLICANT: Kyung, Jin Kim

APPLICANT: Rodrigues, Maria L.

TITLE OF INVENTION: WSX RECEPTOR AG

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
RYAELYVIDVNINISCETDGYLTKMTCRWST
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                        TLLWKPLMKNDSLCSVQRYVINHHTSCNGT
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Pred. No. 0;
; Mismatches
                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                US/08/779,457
COMPUTER: 3.5 inch, 1.44 Mb is COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457 FILING DATE:
                                   PC-DOS/MS-DOS
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100.0%;
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Amino Acid
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 1165, Conservative
                                                                                                                                                                                                                                                                              TYPE: Amin
TOPOLOGY:
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                                      NKDEMMPTTVVSLLSTTDLEKGSVCISDOFN
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LYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV
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US-08-1
Sequence 2, Application US/08780562
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER TEADABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb fl.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/780,562

FILING DATE:
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                                                 08/585005
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
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                                                                                                                    DB
                                                                                                                   Score 6254;
Pred. No. 0;
; Mismatches
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: Amino Acid
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100.0%;
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Matches 1165; Conser
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US-08-780-562-2
                                                                                                                    Query Match
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ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/019003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-6906

TELET: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids
                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 1165; Conservative
                                                                                                                                                  MOLECULE TYPE: protein
FRAGMENT TYPE: internal
S-09-094-410-4
                                                                                                                             TYPE: amino acid
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/590,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569.485
                                                                                                                                                                                                                                                                                                                                APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR ANI
TITLE OF INVENTION: THE DIAGNOSIS AND I
TITLE OF INVENTION: INCLUDING OBESITY P.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                       GLYVIVPVIISSSILLLGTLLISHQRMKKL
                                                                                                                                                            1141 YMPQFQTCSTQTHKIMENKMCDLFV 1165
GEIKWLRISSSVKKYYIHDHFIPIEKYQFS
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04-DEC-1995
MABER: 08/562,663
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08-DEC-1995
                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09094410 GENERAL INFORMATION:
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FILING DATE: 04-DE
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US-09-094-410-4
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHTLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
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ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSED for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/599,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
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STATE: M.
COUNTRY:
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FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELEFOMMUNICATION INFORMATION:
TELEFOMMUNICATION INFORMATION:
TELEFAX: 617-542-8906
TELEFAX: 617-542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: UNROWN
                                                                                                                                                                                                 Query Match 100.0%; Score 6254; Best Local Similarity 100.0%; Pred. No. 0; Matches 1165; Conservative 0; Mismatches
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; FRAGMENT TYPE: internal
US-09-137-132-4
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TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ
US-09-950-149-4
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FILING DATE: <up>APPLICATION NUMBER: US 08/708,123</pr>
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
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COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION NUMBER: US/09/95
FILING DATE: 10-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/59
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/59
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/57
FILING DATE: 11-DEC-1995
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APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/56,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELEPHONE: (617) 542-5070
TELEFHONE: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: (155 amino acids
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            SLYPIFMEGVGKPKIINSFTQDDIEKRQSDA
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APPLICATION NUMBER: US/08/774,414 FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08774414
Sequence 7, Application US/08774414
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
TITLE OF INVENTION: OB PROTEIN RECETTLE OF INVENTION: COMPOSITIONS AN UNMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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MEDIUM TYPE: Floppy disk
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LENGTH: 1216 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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Score 6254;
Pred. No. 0;
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No. 0;
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FILING DATE: 31-DEC-1996
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FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RE
COMPOSITIONS
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Pred.
                                                                        YMPQFQTCSTQTHKIMENKMCDLTV 1165
                                                                               1141 XMPQFQTCSTQTHKIMENKMCDLTV 1165
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ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland D:
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
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SVNFSEAEGTEVTYEDESQROPFVKYATLI
                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/FILING DATE: 27-Sep-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             NAME: Pessin, Karol M. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1216 amino acids TYPE: amino acid
                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                 US-09-671-049-7; Sequence 7, Application US/09671049; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQUS-09-671-049-7
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Matches 1165; Conserv
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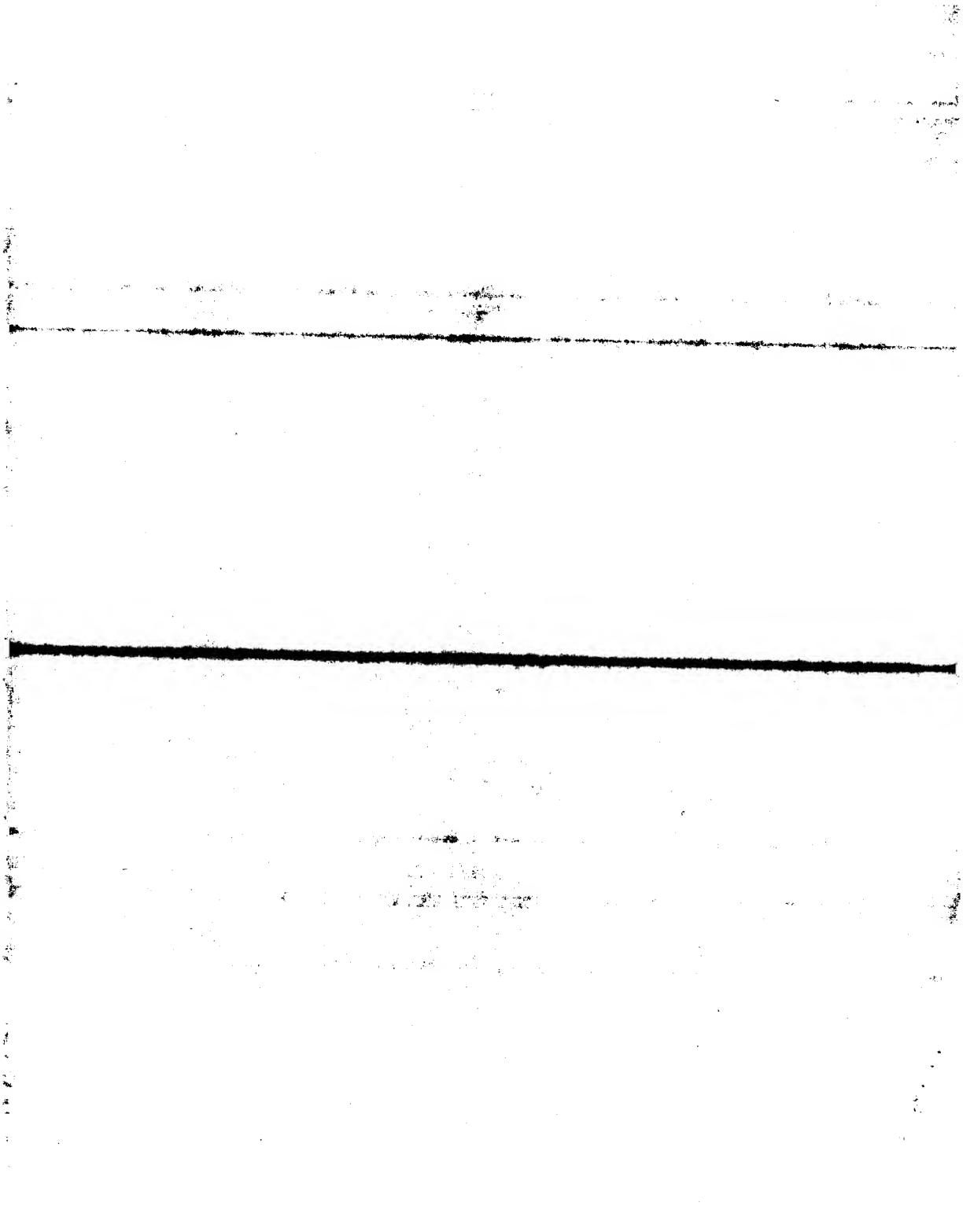
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LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP
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US-09-948-947-87
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APPLICANT: VENTER, J. Craig et al.
IITLE OF INVENTION: POLYMORPHISMS IN KNO
IITLE OF INVENTION: WITH CARDIOVASCULAR
IITLE OF INVENTION: DETECTION AND USES
FILE REFERENCE: CLOO0787;
CURRENT APPLICATION NUMBER: US/09/948,93
CURRENT APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 284
                                                                                                                        Score
Pred.
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Best Local Similarity 99.8
Matches 1163; Conservative
                                                                                       ; TYPE: PRT
; ORGANISM: Human
US-09-948-933-284
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                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/09948947
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH TYPE II DIABETES AND TITLE OF INVENTION: WITH TYPE II DIABETES AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/09/948,947
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FastSeQ for Windows Version 4.0
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6247; D
Pred. No. 0;
2; Mismatches
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                                                                                                                                                                                                                                                                                 Query Match 99.9%;
Best Local Similarity 99.8%;
Matches 1163; Conservative
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US-09-948-947-87
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302	360 362	420	480 482	540 542	600 602	660 662	720 722	780 782	840 842	900	960 962	1020 1022	1080 1082	1140 1142	
)1 GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 	51 VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 111111111111111111111111111111111	21 RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 	31 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 	11 SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV)1 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 	51 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 		31 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 11111	11 GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI)1 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN 	51 SVNFSEAEGTEVTYEDESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPL 	KDSFSNSSWEIEAQAFFI 	31 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS 	11 YMPQFQTCSTQTHKIMENKMCDLTV 1165
24	301	361 363	421	481	5. T.	601	661	721	781	843	901	961 963	1021	1081	114
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Search completed: August 15, 2002, 16:34:03 Job time: 763 sec



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GenCore ver:
Copyright (c) 1993 - 20
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Search time 111.01 Seconds (without alignments) 2425.061 Million cell updates/sec OM protein - protein search, using sw model August 15, 2002, 16:20:55 Run on:

... QTCSTQTHKIMENKMCDLTV 1 MICOKFCVVLLHWEFIYVIT. US-08-779-457-2 6254 Perfect score: Sequence: Title:

1165

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: residues 698052 seqs, 231078099 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending_Patents_AA_New: *

'cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep: * 7654322

predicted by chance to have a score of the result being printed total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

SUMMARIES

		de			SUMMAKLES	
Result No.	Score	Query	Length	DB	ID	Description
	6254	100.0	1165	5	-09-791	Sequence 95040, A
C)	6246	6.66	1165	'n	-791-537-1200	
m	5967	95.4	1163	Ŋ	-09-791-537-1	14096,
4	5941.5	95.0	1194	Ŋ	-791-537-7	_
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Q	4826	77.2	896	Ŋ	-09-791-537-9503	95038,
7	4819.5	•	928	Ŋ	-09-791-537-1	11405
&	4816	77.0	906	រេវា	-09-791-537-1	11405
თ	4814	77.0	968	ហ	-791-537-1	11405
10	4786.5	76.5	1162	Ŋ	-09-791-537-1	
11	4778.5	76.4	1162	S	-09-791-537-	57257,
12	4766.5	76.2	1162	2	1-537-	Sequence 65061, A
13	4766.5	76.2	1174	ហ	-09-791-537	26913,
14	4761.5	76.1	1162	Ŋ	-09-791-537-	53431,
15	4760.5	76.1	1162	ហ	-09-791-537-	45617,
16	4757.5	76.1	1162	ហ	-09-791-537-	91206,
17	4591	73.4	925	ഗ	-09-791-537-	equence 75138,
18	4590	73.4	894	ហ	-09-791-537-	
19	3787	9.09	894	വ	-09-791-537-76	76191,
20	3781	60.5	894	Ŋ	US-09-791-537-11623	11623,
21	3779	60.4	894	Ŋ	S.	_
22	3340	53.4	805	ស	-791-5	
23	3337	53.4	802	5	-537-1	
24	2775	44.4	1148	ល	-537-819	Sequence 8198, Ap
25	2693	43.1	1146	Ŋ	US-09-791-537-126327	
26	1620	25.9	308	Q	US-10-038-010-46	Sequence 46, Appl

Sequence 44, Appl Sequence 42, Appl	Seguence 142984,	Sequence 56948, A	Sequence 26, Appl	Sequence 24, Appl	Sequence 143846,	Sequence 230, App	Sequence 4, Appli	Sequence 9, Appli	Sequence 118267,	Sequence 230, App	Sequence 99945, A	Sequence 7, Appli	Sequence 9, Appli		Sequence 120086,	Sequence 5078, Ap	Sequence 78448, A
US-10-038-010-44 US-10-038-010-42	US-09-791-537-142984	US-09-791-537-5694B	US-09-935-868-26	US-09-935-868-24	US-09-791-537-143846	PCT-US02-19669-230	US-09-853-180-4	US-09-829-472A-9	US-09-791-537-118267	US-10-177-293-230	US-09-791-537-99945	US-09-935-868-7	US-09-935-868-9	US-09-791-537-21626	US-09-791-537-120086	US-09-791-537-5078	US-09-791-537-78448
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US-09-791-537-95040

i Sequence 95040, Application US/09791537

i GENERAL INFORMATION:

j APPLICANT: Bionomix, Inc.

j APPLICANT: Danzer, Joseph

i TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PRO

i TITLE OF INVENTION: METHODS OF USE THEREOF

j FILE REFERENCE: 261/210

i CURRENT APPLICATION NUMBER: US/09/791,537

i CURRENT FILING DATE: 2001-02-22

i NUMBER OF SEQ ID NOS: 153055

i SOFTWARE: Patentin version 3.0

i SEQ ID NO 95040

i LENGTH: 1165
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Pred. No. 0;
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US-09-791-537-95040
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Best Local Similarity
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Query Match
Best Local Similarity 99.9%;
Matches 1164; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-791-537-120058
Sequence 120058, Application US/0979153'
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL:
TITLE OF INVENTION: METHODS OF USE THITIE OF INVENTION OF USE THITIES OF INVENTION NUMBER: US/09/791, CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 120058
LENGTH: 1165
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       361 VPSKEIVWWMNLAEKIPQSQYDVVSDHV
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US-09-791-537-75134
US-09-791-537-75134
Sequence 75134, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 75134
TYPE: PRT
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US-09-791-537-75134
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL ST
TITLE OF INVENTION: METHODS OF USE THER
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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US-09-791-537-14096
; Sequence 14096, Application US/0979153
; GENERAL INFORMATION:
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Best Local Similarity 95.6%;
Matches 1114; Conservative 1
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US-09-791-537-14096
                                                                                                                                                                                                                                                                SEQ ID NO 14096
LENGTH: 1163
TYPE: PRT
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US-09-791-537-95039
US-09-791-537-95039
Sequence 95039, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 95039
LENGTH: 958
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Sequence 114050, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 114050
LENGTH: 958
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larity 94.1%; Pred. No. 0;
Conservative 7; Mismatches
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; ORGANISM: Homo sapiens
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US-09-791-537-95038
; Sequence 95038, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL ST
; TITLE OF INVENTION: METHODS OF USE THER
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 95038
; LENGTH: 896
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                            GASVANFNLTFSWPMSKVNIVQSLSAYPLN
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US-09-791-537-114052
Sequence 114052, Application US/0979153
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL
TITLE OF INVENTION: METHODS OF USE TH
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Belonomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 128089
LIENGTH: 1162
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3-09-791-537-128089
Sequence 128089, Application US/09791537
GENERAL INFORMATION:
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US-09-791-537-128089
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GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL ST
TITLE OF INVENTION: METHODS OF USE THER
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 114053
LENGTH: 896
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Best Local Similarity 99.7%;
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; ORGANISM: Homo sapiens
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US-09-791-537-26913

Sequence 26913, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PRO

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 26913

LENGTH: 1174
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Pred. No. 0;
5; Mismatches
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US-09-791-537-26913
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                                                                     APPLICANT: Bionomix, inc.
APPLICANT: Bionomix, inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL ST
TITLE OF INVENTION: METHODS OF USE THER
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 65061
LENGTH: 1162
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S-09-791-537-65061
Sequence 65061, Application US/09791537
GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-791-537-65061
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Sequence 53431, Application US/097915; GENERAL INFORMATION:

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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 53431
LENGTH: 1162
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-53431
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Pred. No. 0;
6; Mismatches
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Best Local Similarity 75.33
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL ST
TITLE OF INVENTION: METHODS OF USE THEE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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US-09-791-537-45617; Sequence 45617, Application US/09791537; GENERAL INFORMATION:
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                                                 KHTASVTCGPLLLEPETISEDISVDTSWKN
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Run on:

Search time 91.6 Seconds (without alignments) 2200.208 Million cell updates/sec August 15, 2002, 16:22:20;

.....QTCSTQTHKIMENKMCDLTV 1165 US-08-779-457-2 6254 1 MICQKFCVVLLHWEFIYVIT. Title: Perfect score: Sequence:

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residues 562222 seqs, 172994929 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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SUMMARIES

Description	092921 homo sapien	O9mv12 macaca mula	O9my10 macaca mula	002671 sus scrofa	Q92920 homo sapien	092919 homo sapien	рошо	Q13593 homo sapien	Q13594 homo sapien	Q9qwq3 mus musculu	Q9myk9 macaca mula	Q9myll macaca mula	Q9mzs2 sus scrofa	Q62960 rattus norv	Q9ddkl meleagris g	O9iba7 gallus gall
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SEQUENCE FROM N.A.
MEDLINE=98408931; PubMed=9738551;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
"Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA expression in the adipose tissue of normal, hyperinsulinemic, and type 2 diabetic rhesus monkeys.";
Obes. Res. 6:353-360(1998).
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Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF222960; AAF34683.1; -.
HSSP; P16471; 1BP3.
Interpro; IPR002996; CR1A.
Interpro; IPR003961; FN_III.
Interpro; IPR003529; Hematopo_receptor_L_F2.
Interpro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
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                                              GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
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.; Cercopithecidae;
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99MYL0;

01-OCT-2000 (TrEMBLrel. 15, Created)

01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

01-OCT-2001 (TrEMBLrel. 19, Last annotation update)

LEPTIN RECEPTOR LONG INSERT ISOFORM.

Macaca mulatta (Rhesus macaque).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Cercopith
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                                              Cercopithecinae; Macaca
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TISSUE-ADIPOSE TISSUE:
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MEDLINE=98408931; PubMed=9738551;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
Monkey leptin receptor mRNA: sequence, tissue distribution, and m
expression in the adipose tissue of normal, hyperinsulinemic, and
2 diabetic rhesus monkeys.";
Obes. Res. 6:353-360(1998).
                                                                                                                                                                                                                                                                                                                                                                                 GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKENKI
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                                                                                    SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hanse Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF225874; AAF35388.1; -.
EMBL, AF225874; AAF35388.1; -.
HSSP, P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
Receptor.
SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;
                                                                                                                                                                                                                                                                                                                               Length
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Best Local Similarity 93.1
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                             LNSSCVILSWILSPSDYKLMYFIIEWKNLNED
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Sus.
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a; Suina; Suidae;
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annotation update)
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01-JUL-1997 (TrEMBLrel, 04, Created)
01-JUN-1999 (TrEMBLrel, 10, Last seq
01-JUN-2001 (TrEMBLrel, 17, Last ann
TRANSMEMBRANE LEPTIN RECEPTOR.
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MEDLINE-9722487; Pubmed+9069130;
Ernst C.W., Kapke P.A., Yerle M., Ro-
"The leptin receptor gene (LEPR) map:
Mamm. Genome 8:226-226(1997).
EMBL; AF092422; AAC61766.1; -.
EMBL; U72070; AAC48707.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hematopo_receptinterPro; IPR003531; Hematopo_receptinterPro; IPR003531; Hematopo_receptinterPro; IPR003531; Hematopo_receptinterPro; IPR003531; Hematopo_receptinterPro; IPR003531; Hematopo_receptinterPro; IPR03531; 
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                                                                                                                                                                                                                                                             GLYVIVPVIISSSILLLGTLLISHQRMKI
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Cetartlodacty
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID-9823;
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TISSUE-LIVER;
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7
                                Indels
                       Length
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                                Mismatches
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No. 0;
HEMATOPO_REC_S_F1;
                       Score
Pred.
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                       84.3%;
84.0%;
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                           Local Similarity 84.0
nes 980; Conservative
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PROSITE; PS01355;
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FNSVNFSEAEGTEVTYEDESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNS
                               PLKDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIY
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i; Hominidae;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve.
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                   928
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EMBL; U66496; AAB07496.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor
InterPro; IPR003531; Hematopo_receptor
Ffam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
                                                                                           HEMATOPO_REC_L_F2
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MEDLINE-96398968; PubMed-8805376;
Bennett B.D., Solar G.P., Yuan J.Q.
Matthews W.;
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MEDLINE=97215244; PubMed=9061609;
Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
"Cloning and characterization of a human leptin receptor using a
biologically active leptin immunoadhesin.";
J. Mol. Endocrinol. 18:77-85(1997).
EMBL; U66495; AAB07495.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas
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EMBL; U50748; AAC23650.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FW_III.
InterPro; IPR003531; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CRC
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Homo.
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A Cloff1 J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikha Platika D., Snodgrass H.R.;

A Platika D., Snodgrass H.R.;

Platika D., Snodgrass H.R.;

Novel B219/OB receptor isoforms: possible role of leptin in hematopolesis and reproduction.";

hematopolesis and reproduction.";

Nat. Med. 2:585-589(1996).

R EMBL; U52912; AAC50509.1; -.

R HSSP; P16471; 1BP3.

R InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN_III.

R InterPro; IPR003961; FN_III.

R InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003531; Hematopo_receptor_S_F1.

R SMART; SM00060; FN3; 1.

R PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

R PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1.

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1; C7E0E8D18428677B CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                          013592 PRELIMINARY; PRT; 958 AA. 013592; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
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Pred. No. 0;
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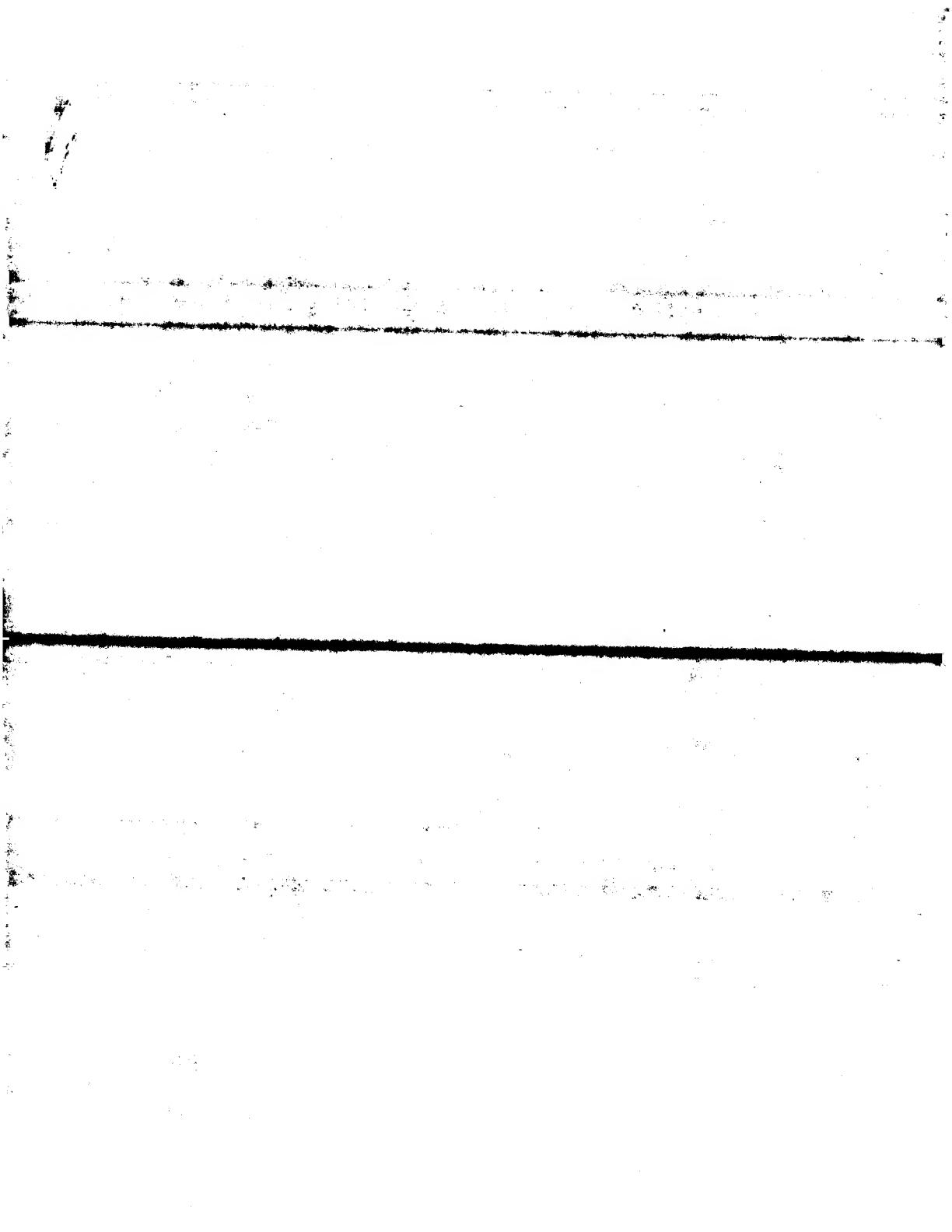
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RESULT 15
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Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31108
A;Reference number: S31108
A;Recession: S31108
A;Recession: S31108
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-119 < RAA>
A;Residues: 1-119 < RAA>
A;Residues: 1-119 < RAA>
A;Residues: i-119 < RAA>
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Reywords: heterotetramer; immunoglobulin homology <IMM> A;Cross-references: EMBL:x62955
A;Note: the nucleotide sequence was submitted to the EMBL Data 1 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM> 밁 γQ Ųγ δõ В QY 멂 Search completed: Job time: 302 sec 닭 Query Match 37.7%; Best Local Similarity 77.3%; Matches 92; Conservative 11 Query Match 37.7%; Score 482; DB 2; Best Local Similarity 77.3%; Pred. No. 2.2e-28; Matches 92; Conservative 12; Mismatches 15 61 \vdash \vdash August 15, 2002, was submitted to the EMBL Data Library, October 1991 Score 482; DB 2; Pred. No. 2.2e-28; 11; Mismatches 16 16:25:02 15; 16; Length 119; Length 119; Indels 0; 0; Gaps Gaps 0; 0;



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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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US-08-463-163-3
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US-09-485-737B-2
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US-08-918-148-79
; Sequence 79, Application
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Result No.

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51.2	51.5	51.5	51.8	51.8	52.0	52.0	52.0	52.0	52.0	52.0	52.0	52.0	52.3	52.3	52.3	52.5	53.1
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4	N	4	N	N	4	N	N	N	N	N	2	N	4	4	4	N	N
US-09-485-737B-91	US-08-403-853-18	US-08-918-148-77	US-08-447-402-1	US-08-553-497A-26	US-09-188-082-16	US-08-661-052-16	US-08-491-988-5	US-08-491-988-7	US-08-491-988-9	US-08-491-988-3	US-08-428-257A-72	US-08-652-507-2	US-09-423-439-51	US-09-423-439-44	US-09-025-769B-178	US-08-797-689-18	US-08-553-497A-22
Sequence 91, Appl	Sequence 18, Appl	Sequence 77, Appl	Sequence 1, Appli	Sequence 26, Appl		Sequence 16, Appl	Sequence 5, Appli	Sequence 7, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 72, Appl	Sequence 2, Appli	Sequence 51, Appl	Sequence 44, Appl	Sequence 178, App		Sequence 22, Appl

ALIGNM ENTS

US/08918148A

Minimum Maximum

Total

on:

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APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibout File Reference: p0979
CURRENT APPLICATION NUMBER: US/08, CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 79
SEQ ID NO 79
RESULT 2
US-08-918-148-74
; Sequence 74, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: artificial US-08-918-148-79
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.3%;
Best Local Similarity 73.2%;
Matches 183; Conservative
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                                                                              FGGGTKLTVL
FGGGTKLTVL
                                                                                                                                                                                                                                                                                                                                    HPGKAPKLMIYEGSKRPSGVSNRFSGSKSGST.
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NPSLKSRVTISVDTSKSQFSLKLSSVTAADTA
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Pred. No.
B; Mismat
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No
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                                                                                                                                                                                                                                                                           VYYCARGRY------FDVWGRGTM 111
                                                                                                                                                                                                                                                                                                                                                                                                 6.5; DB 4; Length 244;
. 3.9e-64;
tches 38; Indels 11; Gaps
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REGISTRATION NUMBER:

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RESULT 3
US-09-079-029-11
; Sequence 11, Application US/09079029
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                                                                                                                                                                                                                                                                                                                                          Patent No. 634200.
Patent No. 634200.
Paneral INFORMATION:
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Best Local Similarity
Matches 171; Conserv
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LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
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                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
ATTORNEY/AGENT INFORMATION: NAME: Marschang, Diane L
                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                 APPLICANT:
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CITY: S
                              FILING DATE: CLASSIFICATION:
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                                                            APPLICATION NUMBER:
                                                                                                                                                                              COUNTRY:
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I: 1 DNA Way
South San Francisco
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Ashkenazi, Avi J.
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Pred. No. 1.8e-61;
); Mismatches 43
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RESULT 4
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Best Local Sin
Matches 170;
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                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marks,
APPLICANT: Schier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schier, Robe: TITLE OF INVENTION: NO. TITLE OF INVENTION: Tume NUMBER OF SEQUENCES: 14: CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
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REGISTRATION
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ADSVKGRFTISRDNSKNTLYLQMNSLRAEDT
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                                                                                                                                                                                                                                                                                              TRY: USA
94111-3834
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             Hunter,
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Two Embarcadero
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66.7%;
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Center, E
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RESULT 5
US-08-646-265A-109
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino
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Best Local Similarity
Matches 164; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6214973
GENERAL INFORMATION:
SOFTWARE: Patentin Release #1.0, Vericurrent Application Data:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/0176:
FILING DATE: 19-OCT-1994
PRIOR APPLICATION NUMBER: JP 5-291078
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN A
TITLE OF INVENTION: MEDULLOBLASTOMA
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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CITY: Washington
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o. 6214973
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3000 K Street,
                                                                                                                                                                                                                                                                                                                                    TSATO, Koh
TSUCHIYA, Masayuki
TSUCHIYA, Masayuki
TRUTION: RESHAPED HUMAN ANTIBODY
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treet, N.W.,
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Pred. No. 3e-56;
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; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: prot US-08-646-265A-109
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acid
                                                                                                                                                                                                                                                                                            APPLICANT: Ashkenazi
APPLICANT: Chunthara
APPLICANT: Kim, Kyun
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)672-5399
TELEX: 904126
                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb 1

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
          NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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STATE: California
                                                                                        FILING DATE:
                                                                                                                                                                                                    COUNTRY: U. ZIP: 94080
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                                                                                                       APPLICATION NUMBER:
TELEPHONE:
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azi, Avi J.
                        Diane L. 35,600
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61.6%;
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No. 6.8e-50;
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DETETISSLQPEDIATYYCQQYNS-YPR 250
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ASVGDRVTITCK-ASQNVG--TNVAWYQ 191
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US-09-079-029-10
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
                                                                                             FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
                                   TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/079,029
                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                        TELEPHONE:
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CITY: South San
STATE: Californi
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TOPOLOGY:
             TYPE:
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5. 6342369
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                   94080
            Amino Acid
                                                                                                                                                                                                                                                                                          California
                       312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         Adams, Camilia W.
Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                              Genentech, Inc.
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                                                                                                                                                                                                                                                                                                        Francisco
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Pred. No. 7.9e-50;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-279-772A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Applica Patent No. 6080560
Query Match
Best Local Similarity
Matches 149; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                         TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                   FILING LALE.

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

NAME: Seay, Nicholas J.

NAME: 27,386
                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772#
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: FU -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 FGGGTKLTVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTA
                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGGGTKLTVL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGOAPVLVIYGKNNRPSGIPDRFSGSSSGNT
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                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box
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Fuller, James T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Quarles and Brady Box 2113
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                                                                                                                                                                                                                                                                                                                                                                                                       of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 734; DB 4; Length 312; ed. No. 3e-49; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                       Version #1.25
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ASLTITGAQAEDEADYYCNSRDSSGNHVV 275
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Conservative

56.0%; 59.4%;

Pred. Score

d. No. 5.9 Mismatches

28.5; DB 3; to 5.9e-49; natches 46;

Length 239;

Gaps

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                                                              Query Match
Best Local Similarity
Watches 149; Conserva
                                                                                                                                           ; MOLECULE TYPE: US-08-902-486-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-902-486-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6140075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                      TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RUSSEL, I
APPLICANT: Fuller, I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: wT
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                                                                                                                                                                                           LENGTH: 239 amino acids
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                                                                                                                                                                                TYPE:
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  61
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                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGM-DVWGQGT 119
                         TLTVSSGGGGGGGGGGGGGQIVLTQSPAIMSASPGEKVTITCSASSS----ISYMHWF
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                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 South Pinckney Street
                                                                          56.0%;
nilarity 59.4%;
Conservative 3
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James T.
METHOD FOR PRODUCING ANTIBODIES
PROTEIN TOXINS IN PLANT CELLS
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                                                                                                                                                                                                                                                             27386
ER: 670513.90261
                                                                       ; Score; Pred. 35; Mis
                                                                        Mismatches
                                                                         > 728.5; DB 4;
. No. 5.9e-49;
ismatches 46;
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                                                                                                 Length 239;
                                                                            Indels
                                                                          21;
                                                                         Gaps
                                                  60
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RESULT 10
US-08-463-163-3
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US-08-463-163-3
                                                                                                ATTOKNEL, ...

NAME: Weber, Ellen ... 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
THE PHONE: (415) 543-9600
                                                       TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TITLE OF I
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                                                                                                                                                                                                                              FILING DATE: 21-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE MEDIUM TYPE: F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
             MOLECULE
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/463,163 FILING DATE: 05-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                               APPLICATION NUMBER: US 07/865,722 FILING DATE: 08-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG--
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94105-1492
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California
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PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATION:
FitzGerald, Davic
Tharv, Vijay K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waldmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaudhary, N
Pastan, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Queen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E ADDRESS:
Townsend and Townsend
e Market Plaza, Steuart
                                                          amino acids
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                                                                                                                                                     015280-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steuart
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Street Tower
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56.0%;

Score

728.5;

DB 1;

Length 599;

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RESULT 11
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
                                                                                                                                                    US-09-423-439-38
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294 
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: .60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.,
STREET: 1100 New York Ave., N.W.
CITY: Washington
                                                                         Local Similarity
mes 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
                                                                                                                                                               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPLTFGSGTKL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQKPGTSPKLWIYTTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCHQ---RST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHWVKQRPGQGLEWIGYINPSTGYTEY
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                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/423,439 FILING DATE: 09-No. 6339070-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                          STRANDEDNESS: single
                                                                        55.5%; larity 55.9%; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.4%;
                                                                         47;
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                                                                        Score 722; DB 4;
Pred. No. 2.3e-48;
7; Mismatches 53;
                                                                                                                                                                  IJ
                                                                                                                                                                  NO:
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                                                                                                     Length 288;
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US-09-423-439-32
; Sequence 32, Applicatio
; Patent No. 6339070
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                     ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ
US-09-423-439-32
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO:
SOFTWARE: MS WOR'D

CURRENT APPLICATION NUMBER: US/09/423,
FILING DATE: 09-NO. 6339070-19
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: PCT/GB98/0
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
FIRING DATE: 673 amino acids
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 142; Conserv
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                                                        NUMBER OF SEQUENCE CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMP
NUMBER OF SEQUENCES: 60
                         VTVSSGGGGGGGGGGGGGSQSVLTQ-PASVSGSPGQSITISCTGTSSDVGG---YNYVS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVSSGGGGSGGGGGGGGDIELSQSPSSL
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                                                                                                                                                                                Conservative
                                                                                                                                                                                              55.5%;
55.9%;
                                                                                                                                                                                 47;
                                                                                                                                                                                              Score 7:
Pred. No
                                                                                                                                                                                                                                                                         ID NO:
                                                                                                                                                                                 Mism
                                                                                                                                                                              722; DB 4; Length 673;
No. 6e-48;
smatches 53; Indels 12; Gaps
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AVSAGEKYTMSCKSSQSLLNSRTRKNYLA 195
                                                                            AVYYCARDRVVVPATSLRGGMDVWGQGTT 120
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                                                           AVYYCARER----AYGYDDAMDYWGQGTT 135
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RESULT 13
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APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurer
TITLE OF INVENTION: Biological Media
FILE REFERENCE: PC9946-A
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                                                                                           Matches
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SEQ ID NO 40
LENGTH: 284
TYPE: PRT
                                                                                                                                                           OTHER INFORMATION: -09-184-658-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(22)
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                          NAME/KEY: SITE LOCATION: (262)..(267) OTHER INFORMATION: His
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                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (271)..
                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (23)..(137)
OTHER INFORMATION: 9A4
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                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                    FEATURE
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                                    WYQQRPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISSVQAEDLAIYYCKQSYTL
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT
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                                                                                                       Similarity
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likely the initiator Met
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                                                                                                                                                                                                                                                                                                                                                                                       domain
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                                                                                          46;
                                                                                                                                                                                                                                                                                                                                   acid linker.
                                                                                        Score 717; DB 3;
Pred. No. 5.5e-48;
6; Mismatches 53
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RESULT 15
US-08-553-497A-20
; Sequence 20, Application U
; Patent No. 5844093
; Patent INFORMATION:
; APPLICANT: KETTLEBOROU;
; APPLICANT: BENDIG, MAR
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OTHER INFORMATION: I
OTHER INFORMATION: I
OTHER INFORMATION: I
US-09-260-527-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Knox, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Willats, W. G.
TITLE OF INVENTION: ANTIBODY
FILE REFERENCE: DYOU19.001AUS
CURRENT APPLICATION NUMBER: US/09,
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Ver.
SEQ ID NO 1
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US-09-260-527-1
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Best Local Similarity
Matches 151; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 280
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTVSSGGGGGGGGGGGGGSQSVLTQ-PASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGGGTKLTVL
                                                                                                                                                                                                                                                                          TTVTVSSGGGGSGGGSGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWY 178
                                                                                                                                                                                                                                                                                                                                      NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQG 118
                                                                                                                                                      R-VFGGGTKLTVL
                                                                                                                                                                                                                            QQHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRST 238
                                                                                                                                                                                                                                                           TLYTYSRGGGGSGGGSGGGGS-SELTQDPAVSVALGQTVRITCQGDS--LRSY-YASWY
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                                                                                                                                      HVVFGGGTKLTVL
                                                                                                                                                                                                 OQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGN
                                                                                                                                                                                                                                                                                                                         DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCARKW ---- RKALR ---- -- WGQG 133
                                                                                                                                                                                                                                                                                                                                                                                    EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGGTT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-homogalacturonan specific antibodies from phage display library known as the Synthetic Library (#1) from the Centre for Protein Engineering, MRC Centre, Cambridge, UK.
                                                                                                                                      262
                                                                                                                                                                  250
                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
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Pred.
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. 9.2e-48;
. ... 52; Indels
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KETTLEBOROUGH,

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US/08553497A

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COUNTR: US
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995

CLASSIFICATION DATA:
APPLICATION UNMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995

PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994

PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994

PRIOR APPLICATION NUMBER: EP 94118970.6
FILING DATE: 17-MAR-1994

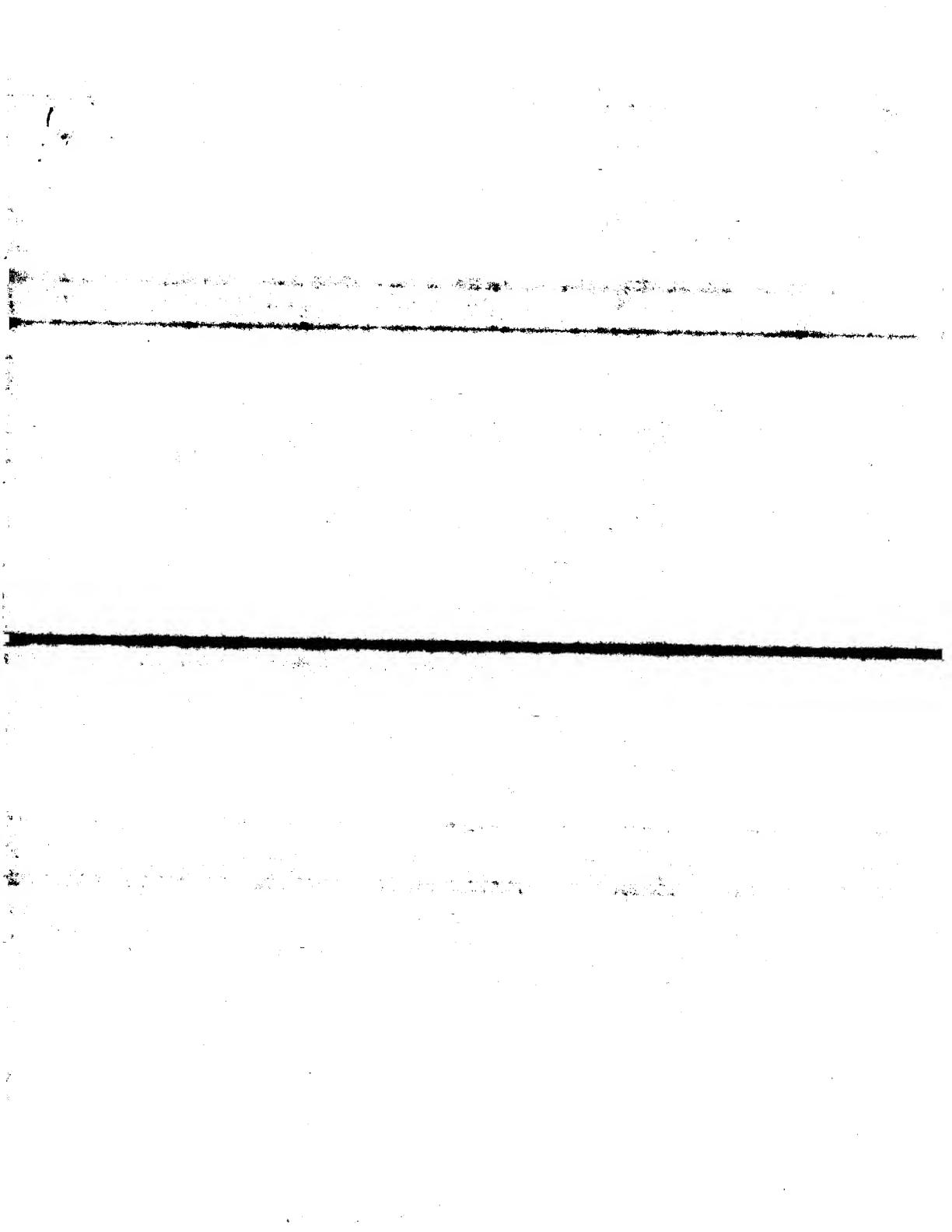
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: BP 94118970.6
FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6333
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APPLICANT: GUSSOW, DETLEF
APPLICANT: MITJANS, FRANSESC
APPLICANT: MITJANS, FRANSESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ATTITEN WHITE ZELANO 6 BRANIGAN, P.C.
231 SSYTTRSTRVFGGGTKLTV 249
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                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 22201
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7:

Db 227 SSYPPMYT--FGGGTKLEI 243

Search completed: August 15, 2002, 16:22:15 Job time: 425 sec



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us-08-779-457

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Copyright (c) 1993 - 2
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OM protein - protein search, using sw model

٠. 90 August 15, 2002, 16:27: Run on:

Search time 111.01 Seconds (without alignments) 520.399 Million cell updates/sec

....SSYTTRSTRVFGGGTKLTVL 250 1 EVQLVQSGAEVKKPGESLKI. US-08-779-457-49 1300 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 698052 segs, 231078099 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

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: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

SUMMARIES

	Description	Sequence 2, Appli	*	_	Ψ	4	Sequence 47, Appl	_	_	127	ш,	51,	43,	43,	19,	Sequence 19, Appl	42,	4	42,	46,	52,	52,	17,	17,	45,	48,	7
SOUTHERS	CI.	US-09-959-373A-2	PCT-US02-16106-16	US-10-151-882-16	US-09-791-537-845	-039-7	US-10-139-785-47	PCT-US02-16106-15	US-10-151-882-15	US-09-791-537-32035	US-10-039-785-51	US-10-139-785-51	US-10-039-785-43	US-10-139-785-43	PCT-US02-16106-19	\vdash	US-10-039-785-42	0-039-785-4	US-10-139-785-42	US-10-139-785-46	US-10-039-785-52	US-10-139-785-52	PCT-US02-16106-17	US-10-151-882-17	US-10-039-785-45	US-10-039-785-48	US-10-139-785-45
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dР	Query Match	89.5	84.0	84.0	77.8	75.4	75.4	74.4	74.4	74.3	74.2	74.2	72.9		•	72.6	٠	٠	٠		72.1		71.9		71.4	71.4	71.4
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	Result No.	1	7	m	4	5	ø	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36

RESULT 2 PCT-US02-16106-16; Sequence 16, Application PC/TUS0216106; GENERAL INFORMATION:

238 VFGGGTKLTVL 248

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Sequence 48, Appl	Sequence 49, Appl	Sequence 49, Appl	Sequence 70804, A	Sequence 73, Appl	Sequence 73, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 14, Appl				Sequence 76, Appl				Sequence 22, Appl
US-10-139-785-48	US-10-039-785-49	US-10-139-785-49	US-09-791-537-70804	PCT-US02-11474-73	US-10-120-414-73	PCT-US02-16106-18	US-10-151-882-18	PCT-US02-16106-21	US-10-151-882-21	PCT-US02-16106-14	US-10-151-882-14	PCT-US02-16106-24	US-10-151-882-24	PCT-US02-11474-76	US-10-120-414-76	PCT-US02-16106-13	US-10-151-882-13	PCT-US02-16106-22
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245	245	245	246	252	252	249	249	241	241	252	252	254	254	253	253	252	252	240
71.4	71.0	71.0	69.5	0.69	0.69	68.89	68.8	65.8	65.8	65.3	65.3	64.3	64.3	64.3	64.3	64.1	64.1	63.6
928	923	923	903	896.5	896.5	894	894	856	856	848.5	848.5	836.5	836.5	836	836	833.5	833.5	826.5
2,2	82	53	30	31	32	33	34	35	36	37	80	<u>6</u>	9	<u>_</u>	12	3	14	51

ALIGNMENTS

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89.5%; Score 1163; DB 5;
Best Local Similarity 89.6%; Pred. No. 2.3e-62;
Matches 225; Conservative 11; Mismatches 11;
                 Sequence 2, Application US/09959373A; General INFORMATION:
APPLICANT: Zardi, Luciano
TITLE OF INVENTION: A tenascin-c isoform as a i; FILE REFERENCE: 1875PT; CURRENT APPLICATION NUMBER: US/09/959,373A; CURRENT FILING DATE: 2001-10-18
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 249
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-959-373A-2
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RESULT 1
US-09-959-373A-2
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                          Factor
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                         Necrosis
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No. 3.5e-58;
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. No. 3.5e-58;
!smatches 17;
                                                                                                                                                                                                                                                                                                                                                                  38;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10151882
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Nec
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 242
ritle Of Invention: Antibodies Against Tumor; FILE REFERENCE: PF54PCT; CURRENT APPLICATION NUMBER: PCT/US02/16106; CURRENT FILING DATE: 2002-05-22; PRIOR APPLICATION NUMBER: 60/293,100; PRIOR FILING DATE: 2001-05-24; NUMBER OF SEQ ID NOS: 48; SOFTWARE: Patentin version 3.0; SEQ ID NO 16; LENGTH: 242; TAVDE.
                        Tumor
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Best Local Similarity 83.6%; Pred.
Matches 209; Conservative 15; Mis
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83.6%; Pred
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PCT-US02-16106-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: A027All scFv US-10-151-882-16
                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 209; Conserv
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US-10-151-882-16
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                                                      AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT
                            SOAFEIWGKGTT
AOKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT
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US-09-791-537-845

US-09-791-537-845

Sequence 845, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 845

LENGTH: 272
                                                                                                                                                                                                                                                                                                                                            OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1012; DB 5;
Pred. No. 2.5e-53;
9; Mismatches 33;
              RESULT 5
US-10-039-785-47
; Sequence 47, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunosp;
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 77.8%;
Best Local Similarity 77.6%;
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens US-09-791-537-845
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PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 47
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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; OTHER INFORMATION: T1014B11 SCFV US-10-039-785-47

61 PQKFHGRVAMTRDTSISTAYMELTRLASDDTAIYYCARQH------HSNTFDPWGQGTL 113 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120 Gaps 1 EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY 60 Length 245; Indels ; Score 980; DB 6; I
; Pred. No. 1.8e-51;
19; Mismatches 32; 75.4%; Score 76.5%; Pred. Conservative Query Match Best Local Similarity Matches 192; Conserva 6 õ 셤 ò 셤

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240 VFGGGTKLTVL 250 234 VFGGGTKLTVL 244 õ

Sequence 47, Application US/10139785; Sequence 47, Application US/10139785; GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that
TITLE OF INVENTION: Receptors

Immunospecifically Bind to TRAIL

TITLE OF INVENTION: RECEPLOIS
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,78
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 47
LENGTH: 245 ; OTHER INFORMATION: T1014B11 scFv US-10-139-785-47 TYPE: PRT ORGANISM: Artificial sequence FEATURE:

61 AQKFQGRVIITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120 Gaps Length 245; 75.4%; Score 980; DB 6; ilarity 76.5%; Pred. No. 1.8e-51; Conservative 19; Mismatches 32 240 VFGGGTKLTVL 250 Query Match Best Local Similarity Matches 192; Conserv 셤 Š 음 g δ 음 ŏ 쉽 ŏ

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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554PCT
CURRENT APPLICATION NUMBER: PCT/US02/16106
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 245 Sequence 15, Application PC/TUS0216106; GENERAL INFORMATION: ORGANISM: Artificial Sequence RESULT 7 PCT-US02-16106-15

Length 245 Query Match 74.4%; Score 967; DB 1; Best Local Similarity 75.8%; Pred. No. 1.1e-50; Matches 191; Conservative 19; Mismatches 32

; OTHER INFORMATION: A004G02 SCFV PCT-US02-16106-15

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                            SSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
SSYGIRWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                            HPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTR-
                                                                                                                                                                                                                                                                                                                                                  Necrosis Factor Delta
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                                                                                                                                                                                                                                                                                                                                                  st Tumor
                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor;
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 245
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US-09-791-537-32035
; Sequence 32035, Application US/097915
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLVQSGAEVKKPGESLKISCQGSGFTF
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US-10-151-882-15
; Sequence 15, Application US/10151882
; GENERAL INFORMATION:
 QVQLVQSGAEVKKPGSSVKVSCKASGGT
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US-10-151-882-15
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                                                                                                                                                                                                                   1111111111
233 SVFGGGTKLTVL 244
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 32035
LENGTH: 254
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US-10-039-785-51
Sequence 51, Application US/10039785
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to T TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-10-09
PRIOR PRIOR PAPLICATION NUMBER: 60/331,310
PRIOR PLICATION NUMBER: 60/331,304
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-00-09-21
PRIOR FILING DATE: 2001-00-02
PRIOR FILING DATE: 2001-00-09-21
PRIOR FILING DATE: 2001-00-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-05
PRIOR PRIOR APPLICATION NUMBER: 60/293,473
PRIOR PRIOR PRIOR OF SEQ ID NOS: 66
SEQ ID NO S1
FENDRE PARENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 254;
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74.3%; Score 966; DB 5;
Best Local Similarity 73.1%; Pred. No. 1.3e-50;
Matches 190; Conservative 19; Mismatches 33.
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                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-32035
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/313,310
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 66
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                                                                                                                                                                                                                                                           EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
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  VIVSSGGGGGGGGGGGGGG-QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ
                                                                                                                                                                                             114 VTVSSGGGGGGGGGGGGGGGGAQSALTQPASMSGSPGQSITISCTGTSSDVGGYNYVSWYQ
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1.5e-49;
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20; Mismatches
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Best Local Similarity 74.6%; Pred. No. 1
Matches 188; Conservative 20; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/10039785
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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US-10-039-785-43
                                                                                                                                                                                                                                                                                                                                                 240 VFGGGTKLTVL 250
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                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                      VTVSSGGGGSGGGGSGGGGS-QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ
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                                                                                                         965; DB 6;
No. 1.4e-50;
                                                                                                                                        ed. NO. 1.40
Mismatches
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TITLE OF INVENTION: Antibodies that Immu TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,78
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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Best Local Similarity 75,3%; Pred.
Matches 189; Conservative 21; Mis
                                                                                                        74.2%; Score
ilarity 75.3%; Pred.
Conservative 21; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/10139785 GENERAL INFORMATION:
; FEATURE:
; OTHER INFORMATION: T1015A07 scFv
US-10-039-785-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: T1015A07 SCFV US-10-139-785-51
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                                                                                                                             Similarity
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LENGTH: 245
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                                                                                                        Query Match
Best Local S
Matches 189
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                                                     113 LVTVSSGGGGGGGGGGGGGGGGAALTQPASVSGSPGQSITISCTGTSSDIGAYKYVSWY
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                                                                                                                                                                                                                                                                                                 APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Imm
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,7
CURRENT APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/323,473
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                     Sequence 43, Application US/10139785 GENERAL INFORMATION:
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0-139-785-43
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188; Conserv
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Matches 188
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                                                                                      Necrosis Factor Delta
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TITLE OF INVENTION: Antibodies Against Tumor Necrosis FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.6%; Score 943.5; DB 1; Best Local Similarity 73.9%; Pred. No. 2.8e-49; Matches 187; Conservative 26; Mismatches 31;
                          GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PF554PCT
CURRENT APPLICATION NUMBER: PCT/USO2/16106
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 248
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US-10-151-882-19
; Sequence 19, Application US/10151882
; GENERAL INFORMATION:
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US-10-151-882-19
                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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ORGANISM: Artificial
FEATURE:
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RESULT 14
PCT-US02-16106-19
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SEQ ID NO 19
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Length 248;

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Score 943.5;

72.68;

Query Match

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Best Local Similarity 73.9%; Pred. No. 2.8e-49;
Matches 187; Conservative 26; Mismatches 31; Indels
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Search time 410.32 Seconds (without alignments) 214.455 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                        3502263 seqs, 351980561
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Maximum DB seq length: 200000000
                                         August 15,
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/cgn2_6/ptodata/2/paa/US101_COMB.pep: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

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SC	ore	Query Match	Query Match Length DB	DB	ID	Description
ָן.	300	100.0		=======================================	11 US-08-779-457-49	Sequence 49, Appl
15	152.5		254	٦	PCT-US01-19110-1412	Sequence 1412, Ap
1152	2.5		254	22	US-09-880-748-1412	Sequence 1412, Ap
1	149	88.4	253	Н	PCT-US01-19110-1813	Sequence 1813, Ap
_	149		253	22	22 US-09-880-748-1813	Sequence 1813, Ap
114	7.5	88.3	252	_	PCT-US01-19110-1666	Sequence 1666, Ap
114	7.5	88.3	252	22	US-09-880-748-1666	Sequence 1666, Ap

Sequence 1880, Ap Sequence 1880, Ap Sequence 1756, Ap Sequence 1756, Ap Sequence 1699, Ap	1770 1770 1450 1450 1746 1746	1397 1397 1397 1661 166 947,	1744 1589 1704 1704 1743 1743 1743	Sequence 1748, Ap Sequence 1748, Ap Sequence 1439, Ap Sequence 1581, Ap Sequence 1581, Ap Sequence 1581, Ap Sequence 1656, Ap Sequence 1656, Ap
1 PCT-US01-19110-1880 22 US-09-880-748-1880 1 PCT-US01-19110-1756 22 US-09-880-748-1756 1 PCT-US01-19110-1699 22 US-09-880-748-1759	PCT-USO1-19110-177 VS-09-880-748-177 PCT-USO1-19110-1455 US-09-880-748-145 PCT-USO1-19110-143 PCT-USO1-19110-143	2 US-09-880-748-13 2 US-09-880-748-13 2 US-09-880-748-13 2 US-09-880-748-16 2 US-09-880-748-16 2 US-09-880-748-94 2 US-09-880-748-94	10-748-174-19110-158-10-158-158-158-158-158-158-158-158-158-170-170-170-19110-174-174-174-174-174-174-174-174-174-174	1 PCT-US01-19110-1748 22 US-09-880-748-1748 1 PCT-US01-19110-1439 1 PCT-US01-19110-1581 22 US-09-880-748-1439 22 US-09-880-748-1581 1 PCT-US01-19110-1656 22 US-09-880-748-1581
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1100	112 113 12 13 13 13 13	222 222 224 237 287	33 33 33 34 35 35 35 35 35 35 35 35 35 35 35 35 35	8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Chiang, Jin Kim
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06/20/96 08/667197
                US-08-779-457-49; Sequence 49, Application US/08779457; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 06/20/96
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RESULT
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bingeries PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1412
LENGTH: 254
TYPE: PATENTAL LONG CANIONS
TYPE: PATENTAL LONG CANIONS
TYPE: PATENTAL LONG CANIONS
TYPE: PATENTAL LONG CANIONS
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Pred. No. 1.1e-86;
14; Mismatches 15;
Pred. No. 1.1e-86; ; Mismatches 15;
            14;
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ilarity 87.4%;
Conservative
  87.48;
 Best Local Similarity 87.4
Matches 221; Conservative
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Matches 221; Conserv
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US-09-880-748-1412
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immuno;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1412
LENGTH: 254
         HELETATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
US-08-779-457-49
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Pred
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 PRIOR APPLICATION DATA:
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241 FGGGTKLTVL 250
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PCT-US01-19110-1666
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                                                                                         Sequence 1813, Application PC/TUS0119110
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
SEQ ID NOS: 3239
SOFTWARE: PatentIN Ver. 2.0
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TITLE OF INVENTION: Antibodies that Immunospecifically Bin FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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13; Mismatches 16.
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241 RVFGGGTKLTVL 252
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Best Local Similarity
Matches 221; Conser
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US-09-880-748-1813
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
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Pred. No. 2.7e-86;
3; Mismatches 13;
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1813
LENGTH: 253
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88.5%; Pre
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1666
LENGTH: 252
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Best Local Similarity 88.5
Matches 223; Conservative
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RVFGGGTKLTVL 250
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. No. 2.7e-86;
ismatches 13;
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US-09-880-748-1666

Sequence 1666, Application US/09880748

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Imm FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,7

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PALENTIN VET. 2.0
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PCT-0S01-19110-1880
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US-09-880-748-1666
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LENGTH: 252
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US-09-880-748-1880

Sequence 1880, Application US/09880748

GENERAL INFORMATION:

TITLE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

PRIOR FILING DATE: 2001-03-25

PRIOR FILING DATE: 2001-03-25

SOFTWARE: PALENTING DATE: 2001-03-25

SOFTWARE: PALENTING DATE: 2001-03-25

SOFTWARE: PALENTING DATE: 2001-05-25

SOFTWARE: PALENTING DATE: 2001-05-25

SOFTWARE: PALENTING DATE: 2001-05-25

SOFTWARE: PALENTING DATE: 2001-05-25

LENGTH: 253
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bin;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1880
LENGTH: 253
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Pred. No. 1.4e-85;
1; Mismatches 17;
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Best Local Similarity 86.9%;
Matches 219; Conservative 14
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1756
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..4e-85;
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                                                      Query Match
Best Local Similarity 86.9%; Pred. No. 1.46
Matches 219; Conservative 14; Mismatches
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immuno;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 87.3%; Pred.
Matches 219; Conservative 12; Mis
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PCT-US01-19110-1756
         ORGANISM: Homo sapiens
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PCT-US01-19110-1756
                   US-09-880-748-1880
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ENGTH: 251
TYPE: PRT
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; Sequence 1756, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR PPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; RIOR FILING DATE: 2001-03-21
; SOFTWARE: PATENTENT VEF. 2.0
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
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2.4e-85;
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Best Local Similarity 87.3%; Pred. No. 2.4
Matches 219; Conservative 12; Mismatches
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NO. 3.9e-85;
-ham 18;
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TILE OF INVENTION: Antibodies that Immunosp;
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1699
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 1699
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87.0%; Pred.
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Best Local Similarity 87.0
Matches 220; Conservative
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Score Pred.

87.2%; 87.0%;

Query Match Best Local Similarity

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Sequence INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1770
LENGTH: 247
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18;
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Pred. No. 7.3e-85;
2; Mismatches 14,
Mismatches
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12;
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llarity 87.3%;
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Best Local Similarity
Matches 219; Conserv
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; ORGANISM: HOMO 8
PCT-US01-19110-1770
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-US01-19110-1770
220;
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236 VFGGGTKLTVL 246

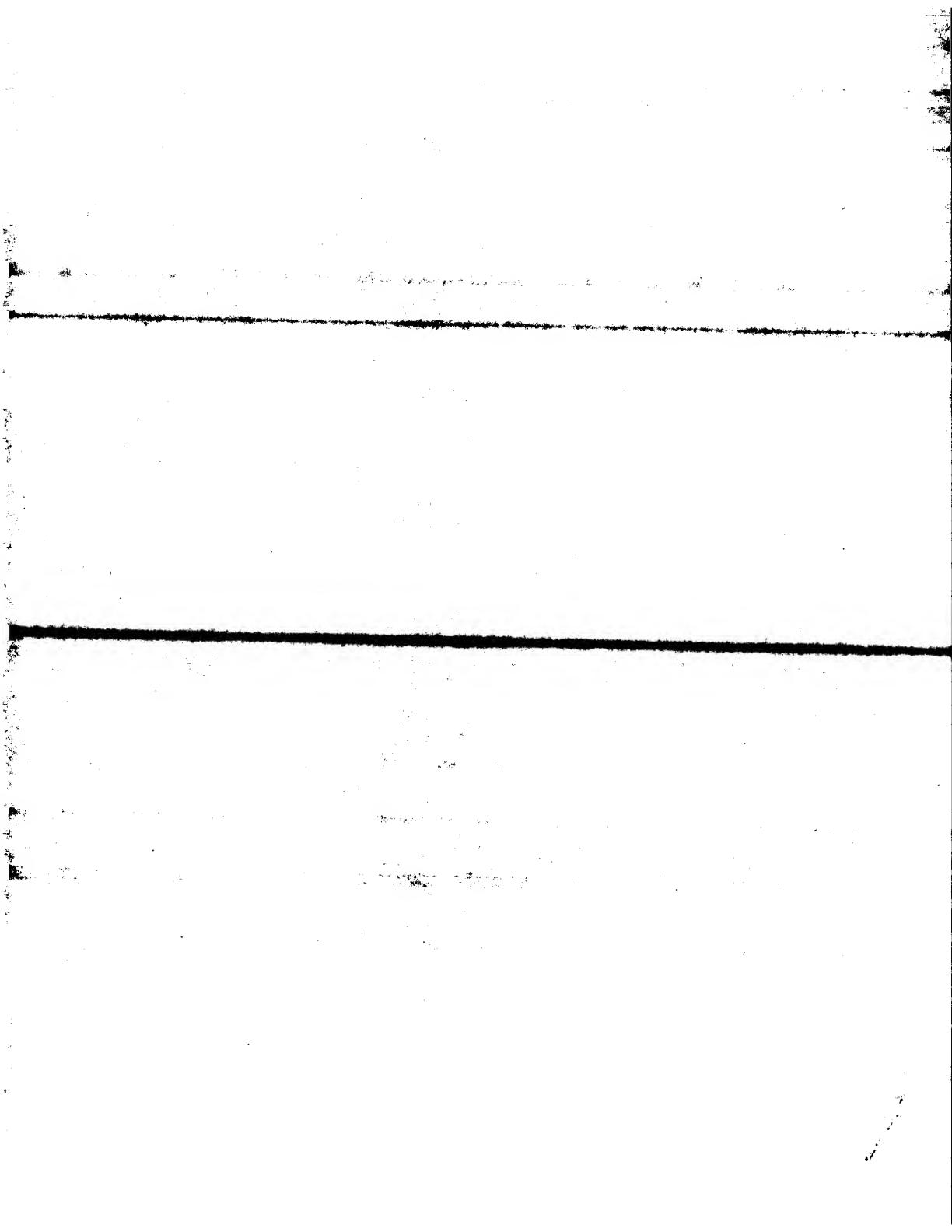
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US-09-880-748-1770
; Sequence 1770, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
; TILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; RIOR FILING DATE: 2001-03-21
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86.9%; Score 1130; DB 22;
Best Local Similarity 87.3%; Pred. No. 7.3e-85;
Matches 219; Conservative 12; Mismatches 14;
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US-09-880-748-1770
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protein search, using sw model OM protein August 15, 2002, 16:24:03; Run on:

Search time 101.13 Seconds (without alignments) 274.582 Million cell updates/sec

.....SSYTTRSTRVFGGGTKLTVL 250 US-08-779-457-49 1300 1 EVQLVQSGAEVKKPGESLKI. score: Sednence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 747574 seqs, 111073796 Searched:

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summar

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Database

A_Geneseq_032802:*

| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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score of the result being printed total score distribution. predicted by chance to have /S1DS1/gcgdata/hold Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

-geneseq/geneseqp-embl/AA2001.DAT:*

SUMMARIES

		•				
Result		* Query				
No.	Score	e Match Length DB	Length	08	ΙD	Description
<b>-</b>	1300	100.0	250	18		Human WSX receptor
C)	1163	89.5	249	21	AAB36083	Recombinant human
m	926.5	71.3	244	20	AAY06718	Antibody 12E10 sin
4	926	71.2	245	22	AAB67618	Human leukocyte an
ιń	918	70.6	245	22	AAB67617	Human leukocyte an
9	907.5	69.8	239	22	AAB69603	Huntingtin intrabo
7	896.5	69.0	243	22	AAG65591	Anti-hEDRF antibod
89	892	68.6	249	20	AAY06713	Antibody 10F6 sing
9	879.5	67.7	304	22	AAG63634	Amino acid sequenc
10	879.5	67.7	304	22	AAG63639	Amino acid sequenc
11	865	66.5	245	22	AAB67619	Human leukocyte an

Single chain Apo-2 Human leukocyte an Human leukocyte an Human leukocyte an Chuman leukocyte an Chuman srv antib Anti-murine CTLA-4 Anti-human CTLA-4 Internalising anti HUMAN SCFV(CEA6)trip H6FXSCFV(CEA6)trip H6FXSCFV(CEA6)trip Anti-platelet glyc Human SCFV1 agains Anti-HIV-1 MAD 447	-1 MAD 44 -1 MAD 44 -1 MAD 44 -1 MAD 44 -1 MAD 44 -1 MAD 44 -1 MAD 44
AAW83324 AAW24061 AAB67621 AAB67623 AAB67622 AAW08487 AAY15127 AAY15127 AAY15127 AAY15127 AAY15127 AAY15125 AAW94269 AAW94269 AAW94269 AAW94269 AAW80381 AAR80391 AAR80399 AAR80384 AAR80385 AAR80385	AAR80394 AAR80394 AAR80395 AAR80396 AAR80397 AAR80387 AAR80378
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### ALIGNMENTS

Human WSX receptor agonist antibody clone #4. standard; Protein; 250 AA (first entry) 17-MAR-1998 AAW24062 AAW24062; AAW24062 

RESULT

Human; WSX receptor; clone #4; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.

Homo sapiens.

W09725425-A1

17-JUL-1997

97WO-US00325 07-JAN-1997; 96US-0667197 96US-0585005 20-JUN-1996; 08-JAN-1996;

(GETH ) GENENTECH INC

Matthews W; Kim KJ, Chiang NY, Carter PJ, Rodrigues ML; Bennett B,

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sapiens
                              20-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                               The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal,
                                                                                                                                                                          especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
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                       to
                                                                                                                                                                                                                                                                                                               Length
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                    WSX receptor and related antibodies and ligands - used products for diagnosis and therapy, e.g. for improving haematopoiesis or for treating tumours
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1.3e-80;
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d. No. 1.
                                                              English
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Pred;
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                                                             Example 14; Pages 121-122; 219pp;
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100.0%;
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WPI; 1997-372864/34
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[gggtk]tv]
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                                                                                                                                                                                                                                                                                                                                  250;
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Best Local S
Matches 250
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The present sequence is a recombinant human antibody scFv. Antibody racts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (cTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agonist antibody; thrombopoletin receptor; TPO-R; thrombopoletin; DIC; megakaryocyte; platelet; immunological; hematopoletic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour;, MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
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                                                                                                                                                                                                                                                                                   Ligands used for diagnosis and treatment of human neoplasias, are capable of identifying the tenascin-C isoform containing domain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
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Pred, No. 2.3e-71;
1; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5-6; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AA
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89.6%;
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19-APR-2000; 2000WO-EP03550
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N-PSDB; AAC67868.
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Best Local Similarity
Matches 225; Conser
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Protein; 245

AAB67618 standard;

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Thu Aug 15 1,6:33:47 2002
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The invention relates to an agonist antibody (Ab) which binds to a thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can thrombopoietin the same way and for the same indications as thrombopoietin (TPO). They can stimulate proliferation, differentiation or growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoietic disorders, especially thrombocytopenia. Thrombocytopenia associated bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia, thrombocytopenia and manne congenital thrombocytopenia, thrombocytopenia myeloablative chemotherapy for treatment of solid tumours or leukaemia, myeloablative chemotherapy for autologous or allogeneic bone marrow transplant, myelodysplasia, allogeneic bone marrow transplant, myelodysplasia, allogeneic bone marrow transplant, myelodysplasia, congenital thrombocytopenia. The antibodies which bind to the MuSK receptor can be thrombocytopenia. The antibodies which bind to the MuSK receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The sequences AAY06718 represent single chain FV (scFV) fragments of sequences alonger half-life than the natural ligand for the TPO-R. Sequences AAY06718 represent single chain FV (scFV) fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody (Ab) which binds to a
                                                                                                                                                                                                                                                                                                                                              nsefnl
                                                                                                                                                                                                                                                                                                                                            antibodies -
                                                                                                                                                                                                                                                                                                                                           New thrombopoietin receptor agonist
treating immunological or hematolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an agonist
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 86pp; English.
                                                                                                                                                                                                                                               Fendly BM
                                                                                             98WO-US17364
                                                                                                                                             97US-0918148
                                                                                                                                                                                                                                             Carter PJ,
                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           various antibodies.
                                                                                                                                                                                                                                                                                           WPI; 1999-204666/17
 WO9910494-A2
                                                                                             21-AUG-1998;
                                                                                                                                             25-AUG-1997;
                                                 04-MAR-1999.
                                                                                                                                                                                                                                            Adams CW,
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244 AA; Sequence

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2
                                                                                                    AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120
                           Gaps
                                                                                                                                                                 EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
                                                                ----fdvwgrgtm
                                                                                                                                                      SGSPGQSITISCIGTSSDVGGYNYVSWYQQ
                                                                                                                                                                                                      STASLTISGLOAEDEADYYCSSYTTRSTRV
                                                                                                                                                                                                                 Length 244;
ore 926.5; DB 20; Lengthed. No. 2.2e-55;
Mismatches 38; Indels
                                                                                                                 npslksrvtisvdtsksqfslklssvtaadtavyycargry
                                                                                                                                                    VTVSSGGGGGGGGGGGGGGUTQPASV
                                                                                                                                                                                                     HPGKAPKLMIYEGSKRPSGVSNRFSGSKSG
71.3%; Score 73.2%; Pred.
                          18;
                         Conservative
             Similarity
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232 fgggtkltvl
             Best Local Sim
Matches 183;
Query Match
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AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The Specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                                                                                                                                 natural killer cell silencing;
                                                                                                                                                                                                                                                    Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_2.
                                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell si
miscarriage; abortion; psoriasis; antibody; HLA phenotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                       in or functional immunoglobulin cyte antigen Cw6, useful for treatment antigen phenotyping -
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                                                                                                                                     natural killer cell silencing;
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                                                                                                           Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_1.
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                                                                                                                                                   HLA phenotyping;
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1. No. 8.1e-55;
4. Smatches 37;
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                                                                                                                                                    antibody;
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                           AAB67617 standard; Protein; 245
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ilarity 72.2%;
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Matches 184; Conser
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                                                                                                                                                    miscarriage;
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            AAB67617
RESULT
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The present invention describes a method for inhibiting the formation of aggregates of certain proteins, involving contacting the protein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCAI), SCA2, SCA3, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody .
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                                                                                                                                                                                                            Parkinson's disease; prion disease; frontotemporal dementla; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2; SCA3; SCA4; SCA5; SCA7; protein accumulation; intrabody
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                                                                                                                                                                                         disorder; Huntington's disease; Alzheimer'
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Pred. No. 4.1e-54;
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                                                                                                                                            SFV.
                                                                                                                                          Huntingtin intrabody alpha-Nt-HD-C4
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21-JUL-2000; 2000US-0620955
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 standard; Protein;
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(MESS/) MESSER A.
(LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF58707
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                                                                                                                                                                                         Neurological
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The invention provides a human erythroid differentiation related factor (hEDRF). The hEDRF polypeptide and the encoding polynucleotide are useful for treating anemias and other erythrocyte deficiencies. The hEDRF protein is useful for producing antibodies, useful in screening assays to identify pharmaceutical compounds of interest and compounds which bind to hEDRF. The polynucleotides are useful for producing hEDRF or its related polypeptides. The antibodies are useful for separating or detecting the corresponding antigen e.g. for detection/quantitation of hEDRF in samples taken from human subjects. Quantification of hEDRF at immunohistochemical level finds value in evaluating the potential of the tissue site to contribute towards the production of new erythroid cells. The present sequence represents the amino acid sequence of an anti-hEDRF antibody
  240
                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human erythroid differentiation related factor and polynucleotides encoding it useful for treating anemia and other erythrocyte deficiencies and for detecting expression of the factor
                                                                                                                                                                                                                                             Human; erythroid differentiation related factor; hEDRF; antianemic; erythrocyte deficiency; antibody ell.
Harriman WD;
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                                                                                                                                           standard; Protein; 243 AA
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                                                   FGGGTKLTVL 250
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                                                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agonist antibody; thrombopoletin receptor; TPO-R; thrombopoletin; DIC; megakaryocyte; platelet; immunological; hematopoletic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour;, MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
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                         45;
             .36-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody 10F6 single chain Fv (scFv) fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL;
                           Mismatches
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896.5;
No. 2.3
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                             AAY06713 standard; Protein; 249 AA
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                          21;
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69.0%;
70.0%;
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                           Conservative
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             Similarity
                                                                                                                                                                                                                                                                                          FGGGTKLTVL
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                          175;
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Query Matc)
Best Local
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        congenital thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for treatment of solid tumours or leukaemia, myeloablative chemotherapy for autologous or allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic anemia, congenital thrombocytopenia, and immune thrombocytopenia. The antibodies which bind to the MuSk receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The antibodies have a longer half-life than the natural ligand for the TPO-R. Sequences AAY06713-Y06718 represent single chain Fv (scFv) fragments of various antibodies.
                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substances with antiviral effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain antibody; ScFv; protein; NS1 protein;
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                                                                                                                                                                                                 Length 249;
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                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; single
CD81; E2
                                                                                                                                                                                                   , DB 20;
4.7e-53;
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No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity determining region; hepatitis C virus; HCV; HCV infective
                                                                                                                                                                                                   68.6%; Score
68.4%; Pred.
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npsfedqvtmsadtsintaylqwsslka:
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                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTITADESTSTAYMELSSLRS
                                                                                                                                                                                                                                                                                                                                                                    HPGKAPKLMIYEGSKRPSGVSNRFSGSK
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 non HIV-induced)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          envelope glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-496986/54
                                                                                                                                                                                                                Similarity
                                                                                                                                                              249 AA;
and
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 (HIV-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                           171;
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Best Local S
Matches 171
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The present sequence represents a single chain antibody of the invention. The specification describes a substance can inhibit the binding between hepatitis C virus (HCV) and cells with potential HCV infection, cells with expression of CD81, or CD81. This substance is especially an antibody with affinity towards HCV E2/NS1 protein, containing amino acid sequences based on the complementarity determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable regions. The antibody inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor. The antibodies and drugs are used for treatment and/or prevention of hepatitis C, or for dlagnosis of hepatitis C.
e.g. antibodies, proteins, sulfated polysaccharides and low-molecular compounds, by inhibiting binding of hepatitis C virus envelope glycoprotein or CD81 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain antibody; ScFv; protein; NS1 protein;
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                                                                                                                                                                                                                                                                                                                                         antibody;
                                                                                                                                                                                                                                                                     Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain variable region of ScFv1-4
                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                    67.7%; Score 879.5; DB 22;
llarity 68.2%; Pred. No. 4e-52;
Conservative 32; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity determining region; CDR; single hepatitis C virus; HCV; HCV infection; CD81; E2 envelope glycoprotein.
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                                                        Disclosure; Page 90-93; 138pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 176; Conser
                                                                                                                                                                                                                                304 AA;
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                                        substances with antiviral effects polysaccharides and low-molecular hepatitis C virus envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell silencing;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .c scFv fragment from clone Cw6_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQPASVSGSPGQSITISCTGTSSDVG-GYN
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tqpssvsqppgqrvtisctgsssnigagyd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen; HLA; HLA-Cw6; natural killer cell siles
ortion; psoriasis; antibody; HLA phenotyping; ss
                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                      Length 304;
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                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                    879.5; DB
No. 4e-52;
smatches 3
                                                                                                                panese
                                       Remedies for hepatitis C containing e.g. antibodies, proteins, sulfated compounds, by inhibiting binding of
                                                                                                             Ja
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGTTVTVSSGGGGGGGGGGGGGGG--QSVI
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                                                                                                                                                                                                                                                                                                                                                    Pred
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                                                                                                             Disclosure, Page 103-105; 138pp;
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68.28;
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Best Local Similarity 68.2
Matches 176; Conservative
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                                                                               glycoprotein or CD81
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2001-496986/54
                                                                                                                                                                                                                                                                                            304 AA;
           N-PSDB; AAH74679
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                                                                                                                                               AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                 Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                                                                                                                                                                                                               SWYQQHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Apo-2; receptor; apoptosis; neurodegenerative disease; tumour necrosis factor; TNF; tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                          66.5%; Score 865; DB 22; Length 245; Larity 68.6%; Pred. No. 3.1e-51; Conservative 18; Mismatches 46; Indels 10
              Ξ
              Kroenke
             Σ
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               Marget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-2 antibody 24C4
                                                                                                                         Claim 3; Fig 1; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 RSTRVFGGGTKLTVL 250
             \hat{\mathbf{z}}
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                   245 AA;
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              Kretzschmar
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Matches 175;
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Sequence
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Best Local
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                                                                                                                                                                                  The present invention describes human Apo-2. Apo-2 can be used
therapeutically to induce apoptosis in mammalian cells, and so is useful
to treat conditions associated with decreased apoptosis e.g. cancer.

Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
(TNFR). TNF cytckines can induce apoptosis, thought to be initiated by
binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
can be used to identify agents activating Apo-2, useful to treat
therapeutically (e.g. those containing immunoglobulin sequences can be
inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
antibodies). It can be used to produce antibodies which can be combined
with a (particularly pharmaceutically acceptable) carrier in compositions
or used to produce dimeric molecules (especially homodimeric molecules
comprising first and second Apo-2 antibodies used to block
single-chain) antibodies can be administered to induce apoptosis in
mammalian cancer cells, and antagonistic antibodies used to block
excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
expression in cells/tissues and in Apo-2 purification. The present
sequence represents a single chain Apo-2 antibody, designated 24C4.
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                                                                                                                              and produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGG---MDVWGQ
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gsrsgtsasla1tglqaedeadyycqsyds-s
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qppsvsgapgqrvtisctgrssnigaghdvhw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                            antibodies to increase or decrease apoptosis
                                                                                                                    useful to
                                                           Х.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 857; DB 20;
ed. No. 1.4e-50;
Mismatches 40;
                                                          Kim
                                                                                                                     apoptosis
                                                         Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVQSGAEVKKPGESLKISCQGSGFT
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adsvkgrftisrdnskntlylqmnslra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Fig 16; 134pp; Englis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.9%; Scor
66.7%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Apo-2 polypeptide inducing conditions linked with decreased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
98US-0020746
97US-0857216
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                                                         Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250
                                  (GETH ) GENENTECH INC
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N-PSDB; AAV72534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 AA;
09-FEB-1998;
15-MAY-1997;
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                                                         Adams CW,
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The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor in an also differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, costeoarthritis, dermatological disorders, hypertension, insulin cresistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aqkfqgrvtmtrdtsigtaymelsrlssddtavyycardryygssayhrgsyymdvwgrg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSX receptor and related antibodies and ligands - used products for diagnosis and therapy, e.g. for improving haematopolesis or for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matthews
Human WSX receptor agonist antibody clone #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Pages 120-121; 219pp; English.
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96US-0585005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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and cholelithiasis
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                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              WO9725425-A1
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08-JAN-1996;
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AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or functional immunoglobulin e antigen Cw6, useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           silencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                scFv fragment from clone Cw6_5
miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human immunoglobulin or functional immifragment specific for human leukocyte antigen Cw6, usof humans and for human leukocyte antigen phenotyping
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No. 1.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               natural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; HLA; HLA-Cw6;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human leukocyte antigen-Cw6 specifi
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                                                                                                                                                                                                                                                                            245 AA
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                                                                                                                                                                                                                                                                          AAB67621 standard; Protein;
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                                                                                                 239 R-VFGGGTKLTVL
                                                                                                                           Query Match
Best Local Similarity
Matches 166; Conser
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                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001
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AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
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113 vtvssagggsgggggggggggggggdieltqppsvsvapgqtariscsg---dalgdkya 169
                                                                                                                                                                                                                                                                                       Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_7.
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                         Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell sile
miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss
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65.9%; Pred. No. 2.9e-48;
ive 23; Mismatches 48;
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Gaps

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-SGGGGSGGGGGGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYV 175

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 15, 2002, 16:36:09; Search time 28.14 Seconds (without alignments) 343.990 Million cell updates/sec

US-08-779-457-49 1300 1 EVQLVQSGAEVKKPGESLKI. Title: Perfect score: Sequence:

......SSYTTRSTRVFGGGTKLTVL 250

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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PRT; 111 AA.	ed) sequence update)	annotation update) NEI.	Craniata; Vertebrata; Euteleostomi;	Catarrhini; Hominidae; Homo.		26;		nocLonal human lambda-type roup II (Bence-Jones protein NEI).":	200	A BENCE-JONES PROTEIN.					Bence-Jones protein; Glycoprotein.	PYRROLIDONE CARBOXYLIC ACID. BY SIMILARITY	N-LINKED (GLCNAC).	**************************************	ADODISOSO4DUG/EB CACU4;	Score 506; DB 1; Length 111; Pred. No. 1.1e-28; 6; Mismatches 8; Indels 0; Gaps	QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGV 200	QSALTQPASVSGSPGQSITISCTGTTSDVGSYNFVSWYQQNPGKAPKLMIYEGNKRPSGV 60	SNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVL 250		PRT; 112 AA.		uence update)	Last annotation update)	Q-1007
STANDARD;	(Rel. 01, Creat (Rel. 01, Last	(Rel. 30, Last	). Chordata;	Primates;	(0006	233223: PubMed=5043326:	., Hilschmann N.;	"The primary structure of a mo- immunoalobulin L-chain of suba	Biochem. 26:10-32(1972	MISCELLANEOUS: THIS IS A B	09; ZMCG.	IPR003006; 19_MHC.	, 0 V C L	IGV; 1.	V region; Benc	106	96	111 111 111 xx. 11501 May.	Š	38.9%; milarity 87.3%; Conservative	OPASVSGSPGOSITISCTGT	QPASVSGSPGQSITISCTGT	GSKSGSTASLTISGLQAEDE		STANDARD;		(Rel. 04, (Rel. 04,	(Rel. 38,	Thain V-II region NIG-84
KESOLT I LV2B_HUMAN ID LV2B_HUMAN	21-JUL-1986 21-JUL-1986 21-JUL-1986	ambda	Homo sapiens (Human Eukaryota; Metazoa;	Mammalia; Euther	[1]	SEQUENCE.	Garver F.A.	"The primar	Eur. J. Bio	-!- MISCELI DIR: A01976	, P017	InterPro; IPR00	InterPro; J	SMART; SMO(	Immunoglobulin	MOD_RES	CARBOHYD	NON_TER	SECOENCE	Query Match Best Local Sin Matches 96;	141 OSVLT	1 QSALT(	201 SNRFS	61 SNRFS	RESULT 2 LV2K_HUMAN ID LV2K_HUMAN	P04209;	20-MAR-1987 20-MAR-1987	15-JUL-1999	י תדבובת הי בו
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                                                                                                                                                               RT myeloma-associated systemic amyloidogenic Bence Jones protein in myeloma-associated systemic amyloidosis.";

RL FEBS Lett. 185:139-141(1985).

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.

DR HSSP; P01709; 2MCG.

OR InterPro; IPR003006; Ig_MHC.

OR InterPro; IPR003596; Ig_W.

OR INTERPROSED SYSTEMIC AMYLOIDS SYSTEMIC AMYLOID
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        Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG lambda chain V-II region VIL.
Homo sapiens (Human).
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Ponsting1 H., Hilschmann N.;
"Structural rule of antibodies. Componocional immunoglobin L chain of tl (Bence Jones protein VIL).";
Hoppe-Seyler's Z. Physiol. Chem. 352-1-MISCELLANEOUS: THIS IS A BENCE-JGPIR; A01977; L2HUVL.
HSSP; P01709; 2MCG.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Bence-Jones DISULFID
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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*** NEDLINE=80114123; PubMed=118915;

*** MEDLINE=80114123; PubMed=118915;

*** A Scholz R., Yang C., Hilschmann N.;

*** Rocholz R., Yang C., Hilschmann N.;

*** Tayle of antibody structure. Primary structure of a human monoclonal

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1 QSALTQPRSVSGSPGQSVTISCTGTSSDVGAYNSVSWYQQHPGKAPKLMIFDVTKRPSGV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-25;
9; Mismatches 13,
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-II region TRO.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 lambda chain V-II region MGC.
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REGION APPEARS TO BE CORRELATED WITH FUTION, 103-THR ABOVE FOR GLY,

MECHANISM IS NOT ALWAYS RANDOM.

THIS CHAIN HAS THE KERN+ AND MCG+
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ight chain dimer crystallized in
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Pred. No. 2.5e-25;
8; Mismatches 14
chain.";
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                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
Edmundson A.B., Ely K.R., Abola E.E., ?
Panagiotopoulos N.;
                                                                                                                                                                                                                              water. Conformational flexibility of a forms.";
J. Mol. Biol. 210:601-615(1989).
-!- MISCELLANEOUS: THE MCG-TYPE C REGION SUGESTING THAT THE V-C JOINING ME SUGGESTING THAT THE V-C JOINING ME -!- MISCELLANEOUS: THE C REGION OF THI
                                                                                                                                     "Rotational allomerism and divergent
immunoglobulin light chains.";
Blochemistry 14:3953-3961(1975).
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                              LAMBDA CHAIN GENES.
MEDLINE-76093781; PubMed-812801;
Fett J.W., Deutsch H.F.;
"A new lambda-chain gene.";
Immunochemistry 12:643-652(1975).
                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY.
MEDLINE-90133913; PubMed-2515285;
Ely K.R., Herron J.N., Harker M.,
"Three-dimensional structure of a
f the Mcg 1-4114(1974)
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PIR, A01975; L2HUMC.
PDB; 2MCG; 15-JUL-92.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Bence
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Best Local Similarity 80.0%;
Matches 88; Conservative
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Biochemistry 13:4102-4
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MEDLINE-75115478; PubMed-804002;

A Medline-75115478; PubMed-804002;

A Medline-75115478; PubMed-804002;

A Indunol. 114:415-421(1975).

C -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.

C -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01972; L2HUBH.

DR PIR; A01972; L2HUBH.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

NW Immunoglobulin V region.

FT MOD_RES 1 BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-II region BO.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.9%; Score 454; DB 1; Length 111; ilarity 80.9%; Pred. No. 3.9e-25; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PYRFSGSKSGNTASLTISGLQAEDEAHYYCCSYAGRFTWVFGGGTNLTVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 SNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01976; L2HUBO.
HSSP; P01709; 2MCG.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
DISULFID 22 90 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94520309932623E8 CRC64;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-II region BOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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LV2I_HUMAN P01712;
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DISULFID
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SEQUENCE
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SEQUENCE
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LV2I_HUMAN
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                                                                                           Gaps
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                                                                                                                                          lata; Vertebrata; Euteleostomi;
rrhini; Hominidae; Homo.
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                                                                                                                                                                                     201 SNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVL 250
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                                                            Length 111;
                                                                                          Indels
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                5A1BF72421BAC CRC64;
                                                                                             14;
                                                                                                                                                                                                                                                                                         LV2A_HUMAN STANDARD; PRT; 111 AA.
P01704;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 01, Last sequence update)
16-JUL-1986 (Rel. 01, Last sequence update)
16-JUL-1986 (Rel. 01, Last sequence update)
16-JUL-1986 (Rel. 01, Created)
16-JUL-1986 (Rel. 0
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ed. No. 6.3e-25;
Mismatches 11;
                                                                           5.4e-25;
                                                             DB 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 lambda chain V-II region BUR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Verte
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Pred.
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11713 MW; FD2
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               92F
                                                                                                                         141 QSVLTQPASVSGSPGQSITISCTGTSSDV
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                                                                             Pred.
                                                                                        10;
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               11785 MW;
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ilarity 76.4%;
Conservative 15
                                                           34.8%;
78.2%;
                                                                                           Conservative
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111
111 AA;
111
111 AA;
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Best Local Similarity
Matches 84; Conser
                                                                           Best Local Similarity
Matches 86; Conser
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P01708;
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DISULFID
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LV2E_HUMAN
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141 QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGV 200
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                                                                                                  MEDLINE-80006606; PubMed-113407; Infante A.J., Putnam F.W.; Infante A.J., Putnam F.W.; "Primary structure of a human IgAl immunoglobulin. V. Amino acid sequence of a human IgA lambda light chain (Bur)."; J. Biol. Chem. 254:9006-9016(1979).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-II region WIN,
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
APPEARS TO BE A FREE BUT UNREACTIVE SULFHYDRYL GROUP.
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MEDLINE=79062503; PubMed=102365;
Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
"Amino acid sequence of the human myeloma lambda chain Win.";
Biochim. Biophys. Acta 537:9-21(1978).
-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 SNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVL 250
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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HSSP; P01709; 2MCG.

InterPro; IPR003506; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

Immunoglobulin V region; Bence-Jones protein.

MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

DISULRID 22 90 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
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Pred, No. 7.8e-24;
7; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.5%;
78.2%;
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HSSP; P01709; 2MCG.
InterPro; IPR003006; Ig_MHC
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                  Fram; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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109 AA;
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Best Local Similarity
Matches 86; Conser
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MEDLINE-71064024; PubMed-5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
                                                QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGV 200
                        Gaps
                                                              1 QSALTQPPRVSGSPGQSVTISCTGSYSNVTGYNHVSWYQQDPGKVPKLMIYDVDKRPSGV 60
                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-I region EU.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                    420; DB 1; Length 117;
No. 9.1e-23;
                                                                                                     201 SNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTRVFGGGTKLTVL 250
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                        Indels
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No. 1.8e-23;
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MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immun Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
-!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 (
MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
PIR; A02023; G1HUEU.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SMO0406; IGV; 1.
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Mismatches
         Pred. No. 1.8(); Mismatches
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65.9%; Pred. N
tive 12; Mism
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                      10;
        75.5%;
                       Conservative
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117
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Best Local Similarity
          Similarity
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P01742;
                      83;
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          Best Local
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                       Matches
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A Takayasu T., Takahashi N., Shinoda T., Okuyama T., Tomioka H.;

Takayasu T., Takahashi N., Shinoda T., Okuyama T., Tomioka H.;

Tomparative studies on the structure of the light chains of human immunoglobulins. III. Amino acid sequence of a lambda type Bence J., Biochem. 89:421-436(1981).

B PIR; A01979; L2HU58.

R HSSP; P01709; 2MCG.

R InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

R Ffam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

I PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKRPSGV 200
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
(VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG heavy chain V-I region HG3 precursor.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 JuL-1999 (Rel. 38, Last annotation update)
19 Jambda chain V-II region NIG-58.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 411.5; DB 1;
Pred. No. 3.3e-22;
4; Mismatches 22;
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75.5%;
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110 AA;
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P01743;
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EMBL; X01147; CAA25598.1; -.

DR PIR; A01966; LiHUBL.

DR HSSP; P01703; 7FAB.

BR HSSP; P01703; 7FAB.

DR HSSP; P01703; 7FAB.

BR HSSP; P01703; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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"Molecular cloning of a human immunoglobulin lambda chain variable
sequence.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                        IG HEAVY CHAIN V-I REGION HG3
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                                                                                                                                                                                                                                                                                                                                            401; DB 1; Le
No. 1.8e-21;
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2.6e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AOKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCAR 98
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-I region BL2 precursor.
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. No. 2.6e
!smatches
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Mismatches
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Best Local Similarity 65.2%; Pred.
Matches 75% Conservative 20; Mis
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                                                                                                                                      Signal
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77.6%;
    Ig_MHC.
Ig_v.
InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; S:
SIGNAL 1 19
CHAIN 20 117
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117
117 AA;
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Best Local Similarity
Watches 76; Conserv
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GGGSQSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEGSKR 196
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                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-I region V35 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PIR; S00476; HVHU35.

InterPro; IPR003006; Ig_MHC.

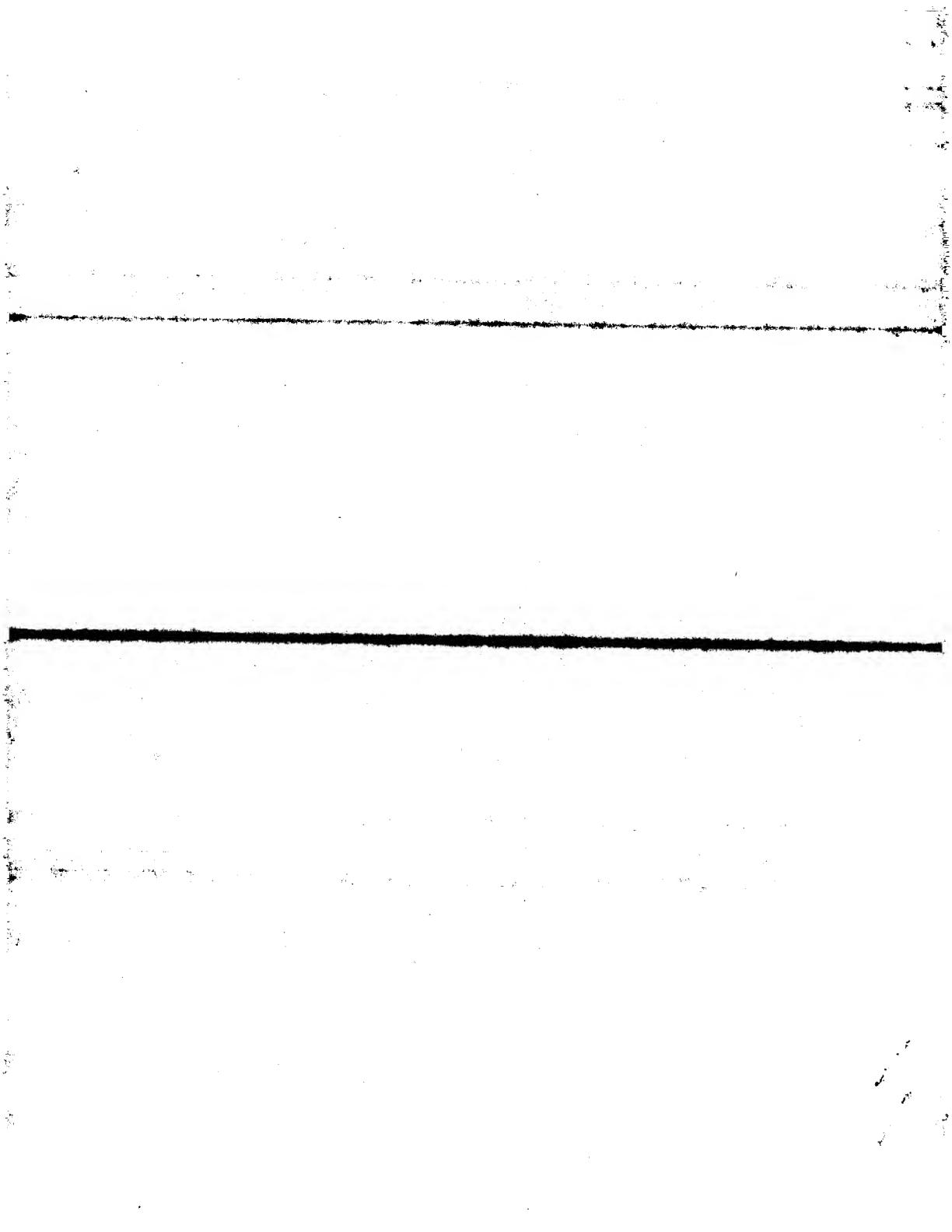
InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

Immunoglobulin V region; Signal.
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117 AA;
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                                                                                                          Search time 91.6 Seconds (without alignments) 472.148 Million cell updates/sec
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Maximum Match 100%
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sp_bacteria:*
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb;
6: sp_mammal:*
7: sp_mhc:*
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                        Euteleostomi; Murinae; Mus
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MEDLINE-98170165; Pubmed-9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee.
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of cDNAs encoding VH and VL monoclonal anti-CEA antibody (CEA 79) cross-reactive with generation of a single-chain FV molecule (scFV).";
Mol. Cells 7:816-819(1997).

EMBL; U88067; AAB48047.1; -.
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0921A6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae;
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ed. No. 1.1e-41;
Mismatches 64;
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241 AA; 26086 MW;
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Matches 134; Conservative 33
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STRAIN-BALB/C;
Cui D., Zeng G., Yan X., Li X., Su C.;
Cui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repairing of intestinal RNA of mice of of the irradiated mice by treatment with the intestinal RNA of mice of the irradiated mice by treatment with the intestinal RNA of mice of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240168; AAK43733.1; ..
NON_TER 218
SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRYTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT
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Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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09UL92;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
   Created)
Last sequence update)
Last annotation update)
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Pred. No. 7.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 QQKPGQPPKLLIYAASKQGSGVPAGLLASGSGTDFSLNI 214
                                                                                                                                                                                                                                                                                              Ren
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EMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 QOHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTI
                                                                                                                                                                                                                                                                                           Tian F.,
                                                                                                                                                                                                                                                                                             .
[24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
                                                                                                                                                                                                                                                                                                D., Zeng G., Yan X., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.7%;
illarity 52.1%;
Conservative 38
01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                 MRP5 (FRAGMENT).
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09UL95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCA-----SSNWGPYWYFDLWGRGTL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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                                                                                                                                                             1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                           1 EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                               (rragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                      Length
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                                                          1BAAACBD96ACD2A2 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                     ; Score 461.5; DB 4;
; Pred. No. 4.4e-28;
10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 450.5; DB 4;
Pred. No. 2.8e-27;
9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                           -192(1998)
                                                                                                                                                                                                                                                                      A.
                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                               fetus.";
Clin. Immunol. Immunopathol. 87:184-1
Clin. AF035025; AAD56261.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                    Query Match
Best Local Similarity 74.6%; Pred.
Matches 94; Conservative 10; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.7%; Score 72.8%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
12605 MW;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 124 124
SEQUENCE 124 AA; 13580 MW;
                                                          13580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.8
Matches 91; Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AA;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                    120 TVTVSS 125
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VTVSS 116
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NON_TER
SEQUENCE
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09UL89;
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Q9UL89
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
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د
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.M.,
                                                                                                                                                                                                                                                                                           "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAKB2649.1; -.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
Young D.C.;
                                                                                                                                                           Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09UL95;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
9960S0 PRELIMINARY; PRT; 159 AA. 0960S0; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%; Score 450.5; DB 4; Best Local Similarity 67.7%; Pred, No. 4e-27; Matches 88; Conservative 17; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87
EMBL; AF035019; AAD56255.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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13516 MW;
                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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125 AA;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Tilson M.D.;
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AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120
                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                119
13205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                119 AA;
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGTTVTVSS 125
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                                                                                              NCBI_TaxID-9606;
                     (FRAGMENT)
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NON_TER
SEQUENCE
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STRAIN-BALB/C;
Cui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of
                                                                                                                                                    AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120
                                                                                                                                                                          |||||||||||||| : : ||:||||||
|DTAVYYCARSQGGRIAAAGDAFDIWGQGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AOKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGG---MDVWGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 NQKFKGKATMTVDKSSITAYMELARLTSDDSAIYYCARG-----AYYGSFYYFDYWGQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                            SSYKMNWVRQAPGKGLEWMGGIIPIFGTANY 60
                                                                                              their precursors improving irradiation in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phys. Chem. Med. 19:71-80(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tian F., Ren D., Zhao T., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 170;
 Length 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2823CC6C10F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 2.1e-25;
smatches 31;
DB 4;
1.3e-25;
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                                                                                                                                                                                                                                                                                                                                                             170 AA
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                                    smatches
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No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 33.0%; Score Best Local Similarity 53.8%; Pred. Matches 85; Conservative 23; Mis
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                    14; Mi
                                                                          1 EVQLVQSGAEVKKPGESLKISCQGSGFTF
                                                                                              the same strain.";
Int. J. Radiat. Biol. Relat. Stud.
EMBL; AF240167; AAK43732.1; -.
SEQUENCE 170 AA; 17978 MW; 504
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33.0%; Score
                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C;
Cui D., Zeng G., Yan X., Wang F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 GTTVTVSSGGGSSGGGSGGGSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Q925S2;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                   66.48;
                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                   Similarity
                                                                                                                                                                                                                                                              121 VTVSS 125
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09UL94;
01-MAY-2000 (
01-MAY-2000 (
      Vuct.
Best Local Simi
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           Euteleostomí;
                                                                                                                                                                                               MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%; Pred. No. 1.5e-25;
Matches 86; Conservative 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 428; DB 4; Length 614; llarity 32.0%; Pred. No. 1e-24; Conservative 31; Mismatches 82; Indels 1
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13E64F5345F4A16E CRC64;
                                                                           Craniata, Vertebrata, F
Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096GA6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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172 YASWYQQKPGQAPVLVIYGKNN----RPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY
          D., Zeng G., Yan X., Wang
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Best Local Similarity
Matches 112; Conserv
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                                                                            SEQUENCE FROM N.A.
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096GA6
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                                                                            EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                      "Homo sapiens putative microfibrillar protein with Ig-like domain mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAK82649.1; -.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                        Euteleostomi;
Homo.
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                                 Length 124;
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1BAAACBD96ACD2A2 CRC64;
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on update)
                                                                                                                                                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 479.5; DB 4;
No. 7.8e-32;
ismatches 20;
                                 core 491.5; DB 4;
red. No. 6.1e-33;
Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                   rrhini;
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Llarity 72.5%; Pred.
Conservative 11; Mis
                                 Score
Pred.
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Mammalia, Eutheria, Primates, Cata
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13580 MW;
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                                 37.0%;
75.8%;
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SEQUENCE FROM N.A.
124 AA;
                                          Local Similarity
hes 97; Conser
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WGQGTTVTVSS
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092582;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Best Local Sim
Matches 95;
                                  Query Match
SEQUENCE
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0960s0;
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STRAIN-BALB/C;
Cui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                           "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                    the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240167; AAK43732.1; -.
SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC009851; AAH09851.1; -.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 63.4%; Pred. No. 9.3e-32;
Matches 90; Conservative 17; Mismatches 29;
   Ren
Tian F.,
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                                                                   Gaps
                                                                                           1 ELTQDPVVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                           09UL95 PRELIMINARY; PRT; 125 AA.
09UL95;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2001 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                  Length 107
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                  GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVL 249
                107 107
107 AA; 11306 MW; A2B04B37187A5F00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                Kalis N.N., Berney
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                  Score 546; DB 4; I
Pred. No. 1.8e-37;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
12;
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Pred. No. 2.2e-37;
9; Mismatches 12
                                                                                                                                                                                                                                                                                                                               -192(1998)
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                                                                                                                                                                                                                                                                                                                    fetus.";
Clin. Thunnol. Immunopathol. 87:184-1.
CMBL; AF035019; AAD56255.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
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                                                  Score
Pred.
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Best Local Similarity 81.9%; Pred.
Matches 104; Conservative 9; Mis
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
"Myosin-reactive autoantibodies in
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13516 MW;
                                                  41.18;
98.18;
                                                                  Conservative
SM00406; IGV; 1.
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125 AA;
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Best Local Similarity
Matches 104; Conser
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TMVTVSS
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WEDLINE*98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.;
                                                                                    Homo sapiéns (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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                                                                                                                                                                                                                                                                                                                          fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
NON_TER 119 119
SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E C
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Pred. No. 5e-36;
7; Mismatches
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EMBL; AF035022; AAD56258.1; -.

HSSP; P01772; 2FB4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; 19; 1.

SMART; SM00406; IGV; 1.
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llarity 81.9%;
Conservative 7
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Best Local Similarity
Matches 104; Conser
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-98170165; PubMed-9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain Fv molecule (scFv).";
Mol. Cells 7:816-819(1997).
EMBL; U88067; AAB48044.1; -.
NON_TER 1 1 1
NON_TER 241 241
SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;
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                                          TLVTVSSGGGGTGGGGSGGGGSS-ELTQDPA-VSVALGQTVRITCQGDSLRSYYASWYQQ
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Sciurognathi; Muridae; Murinae; Mus
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on update)
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0921A6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Manmalia; Eutheria; Rodentia; Sciurognathi; Murida
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5.6e-45;
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52.2%;
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Best Local Similarity
Matches 133; Conserv
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Cui D., Zeng G., Yan X., Li X., Su C.;
Cui D., Zeng G., Yan X., Li X., Su C.;
Cui D., Zeng G., Yan X., Li X., Su C.;
Cloning of mouse genes related to repairing of intestinal epitheli
of the irradiated mice by treatment with the intestinal RNA of mice
the same strain.";
Lint. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240168; AAK43733.1; -.
NON_TER 218
SEQUENCE 218 AX; 23013 MW; 527E4FABF7982817 CRC64;
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Sciurognathi; Muridae; Murinae; Mus
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L43092; AAA69746.2; -.
HSSP; P01709; 2MCG.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig: 1.
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Pred. No. 8.9e-39;
39; Mismatches 56
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                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia;
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nilarity 50.2%;
Conservative 39
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19,
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Best Local Similarity
Matches 111; Conserv
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TISSUE-LYMPHOCYTE;
Hobmann A.;
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## ALIGNMENTS

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090; SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
MEDLINE-20183931; PubMed-10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."; Length 298 E0F96B8A17004317 CRC64; Created) Last sequence update) Last annotation update) 97:2585-2590(2000) method.";
Proc. Natl. Acad. Sci. U.S.A. 97
EMBL; AB036341; BAA88633.1; -.
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V. Q9QYF0 Q9QYF0; Q1-MAY-2000 (TrEMBLrel. 13, C: 01-MAY-2000 (TrEMBLrel. 13, Li 01-DEC-2001 (TrEMBLrel. 19, Li CN 8 SCFV. Pfam; PF00047; 19; 2.
SMART; SM00406; IGV; 2.
SEQUENCE 298 AA; 31867 MW;

Gaps 23; Indels Ouery Match 48.7%; Score 647.5; DB 11; Best Local Similarity 50.2%; Pred. No. 3.1e-45; Matches 128; Conservative 36; Mismatches 68;

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;; virucidal; antibacterial; TF antigen;
                                                                                           The present sequence is that of human single chain antibody (scFv)

HID-1, which is directed against platelet glycoprotein ID (GPID).

HID-1 is composed of a heavy chain variable region (see AAY95189)

and light chain variable region (see AAY95194)

clinker. The HID series of scFv was isolated from a human synthetic vH and VL scFv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID alpha component of the GPID/IX/V complex on their surface, followed by a 4th round of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scFv from washed platelets by flooding with murine monoclonal antibody or mimotope peptide (see AAY95229). Whether displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation
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This invention describes a novel vaccine (VI) against

conformation-dependent antigens (CDA) comprising DNA (I) and/or an
autibody, or peptide which immunologically imitates CDA, is new. (I)
cencodes a region of an antidiotypic antibody (Ab2) or another peptide
which: (a) specifically binds to the binding site of an antibody (Ab1)
cencodes a region of an antidiotypic antibody (Ab2) or another peptide
which: (a) specifically binds to the binding site of an antibody (Ab1)
cor an antigen binding molecule; and (b) immunologically mimics the
initial antigen. The epitope is partially or completely
conformation-dependent, and has an immunogenic structure defined by a
specific spatial conformation of amino acids. (I) is used in the form
of linear or circular naked DNA and/or with a viral vector and/or
adjuvants. The products of the invention have cytostatic, virucidal,
adjuvants. The products of the invention have cytostatic, virucidal,
antibocterial and antiparasitic. The invention also describes (I) a
corresponding vaccine (V2) against antigens which are not proteins or
peptides, as defined above but which have epitopes which show an
immunogenic structure; (2) preparing (V1) and (V2); (3) human
corresponding vaccine (V2) against the MUCl-conformation epitope
having one of 31 approximately 60 residue amino acids sequences, all fully in the
specification; (5) antidotypic antibody fragments against the TF
chaving one of 16 9-17 residue amino acid sequences, all fully in the
specification; (5) antidotypic antibody fragmentes against the TF
antigen having one of 24 approximately 200 residue amino acid sequences,
fully defined in the specification; (6) TF carbohydrate epitope mimetics
thaving one of 25 7-13 residue amino acid sequences, all fully defined
the specification; and (17) DNA sequences encoding the fragments and
cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
and parasites. The procious diseases, e.g. caused by prions, viruses defined the procious viruses, backer of the procious diseases
                                                                                                                                                                                                                                                                        based
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines against conformation-dependent or non-peptide antigens, on DNA encoding peptide which mimics the antigen, useful e.g. as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.2%; Score 907; DB 22; Length 2 Ilarity 70.0%; Pred. No. 7e-54; Conservative 28; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|| |::|| : : |:::: | ::||||||||| ::
adsvkgrftisrdnaknslylqmnslraedtavyycardpfh----
                                                                                                                                   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 13; 36pp; German.
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                                                               99DE-1024405
99DE-1043016
                                                                                                                                                                                  Karsten U;
                                                                                                                                                                                                                              WPI; 2001-049937/06.
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Best Local Similarity
Matches 175; Conserv
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                                                                27-MAY-1999;
09-SEP-1999;
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                                                                                        29-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller JL;
                                                                    AAY95198;
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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Region
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                          14
                                   AAY951
                                                                    <del>ب</del>
                                                                                                                                                                                                                                                     The present sequence is that of human single chain antibody (scFv) HID-3, which is directed against platelet glycoprotein Ib (GPIb).

HID-3 which is directed against platelet glycoprotein Ib (GPIb).

HID-3 is composed of a heavy chain variable region (see AAY95210)

and light chain variable region (see AAY95215) joined via a peptide
linker. The HID series of scFv was isolated from a human synthetic
VH and VL scFv library by 3 rounds of phagemid selection against
transfected CHO cells expressing the GPIb alpha component of the
GPIb/IX/v complex on their surface, followed by a 4th round of
selection against washed human platelets, and 2 final rounds in
Which attempts were made to displace scFv from washed platelets by
flooding with murine monoclonal antibody or mimotope peptide (see
AAV95229). Whether displayed as surface proteins on a phagemid or
secreted as free scFv by Escherichia coli, the HID scFv clones are
capable of inhibiting von Willebrand factor-dependent aggregation of
platelets. The scFv are composed of native human protein sequences
and are therefore attractive potential reagents for therapeutic
purposes. They provide a new class of antithrombotic agents,
useful for the prevention of platelet-dependent thrombi in
diseased arteries, bypass grafts, dialysis etc., and can also be
used as diagnostic reagents. Methods of inhibiting aggregation
of platelets, of binding human platelet GPIb alpha and of selecting
a VH or VL region of an antibody that inhibits platelet aggregation
                                                                                                                                                                                       Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet aggregation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 926; DB 21;
Pred. No. 3.7e-55;
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25; Mismatches
227..237
/note= "framework region
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adsvkgrftisrdnskntlylqmnslraed
                                                                                                                                                                                                                                    Disclosure, Fig 7; 89pp; English
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                                                                             99WO-US25495
                                                                                                  98US-0106275
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                                                                                                                        (MILL/) MILLER
                                WO200026667-A1
                                                                                                  30-OCT-1998;
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                                                       11-MAY-2000
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                                                                                                                                             Miller JL;
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Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet aggregation .
                                                                                                                                             scFv; human; HIb-1; glycoprotein Ib alpha;
antiaggregant; antithrombotic; thrombus;
                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 1"
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/note= "heavy chain variable region"
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/note= "complementarity determining
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/note= "complementarity determining
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/note= "complementarity determining
                                                                                                                Anti-platelet glycoprotein Ib human scFv HIb-1.
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e= "vector-derived linker"
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.te= "light chain variable
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te= "framework region 4"
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/note= "framework region 1"
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/note= "framework region 2"
179..185
                                                                                                                                                                                                                                                                                                            ...30
'note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...238
te= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                           15..49
'note= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity
                                                                                                                                                                                                                                                           Location/Qualifiers
198
AAY95198 standard; Protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0106275
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                                                                                                                                                                                                             Chimeric - Homo sapiens.
Chimeric - synthetic.
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/note=
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/note=
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114..13
                                                                                                                                               Single chain antibody;
                                                                                                                                                               platelet; aggregation;
therapy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                           /note=
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conformation-dependent antigens (CDA) comprising DNA (1) and/or an antibody, or peptide which immunologically imitates CDA, is new. (T) encodes a region of an antidiotypic antibody (Ab2) or another peptide which immunologically imitates CDA, is new. (T) encodes a region of an antidiotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an antigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form of linear or circular naked DNA and/or with a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) human antidiotypic antibody fragments against the MCC1-conformation epitope mimics having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (6) residue amino acid sequences, antigen having one of 24 approximately 200 residue amino acid sequences, the specification; (6) artidiotypic antibody fragments against the TF candon or the specification; (6) TF carbohydrate epitope mimetic candigor and or 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetic cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasites. The vaccines are effective in cases where vaccination has
                                                                                                                                                                                                 lependent antigen; antibody; cancer;
virucidal; antibacterial; TF antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endent or non-peptide antigens, based ics the antigen, useful e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine (V1) against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIZIN MAX.
                                                                                                                                                                                               MUC1; human; vaccine; conformation-dependent antiidiotypic antibody; cytostatic; virucidal antiparasitic; infectious disease.
                                                                                                                                                            Human TF ant1-idiotype antibody fragment K2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    man.
                                   AAB46052 standard; Peptide; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccines against conformation-depe
on DNA encoding peptide which mimi
antitumor vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DELB-) DELBRUECK CENT MOLEKULARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 12-13; 36pp; Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and parasites. The vaccines a previously not been possible.
                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-DE01809
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99DE-1043016
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                                                                                                                                                                                                                                                                                                                       WO200073430-A2
                                                                                                                                                                                                                                                                                   Homo sapiens.
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09-SEP-1999;
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                                                                                                                    23-MAR-2001
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                                                                              AAB46052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goletz
                   AAB46052
RESULT
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Length 240;

936; DB 22; No. 7.9e-56;

Score Pred.

70.48;

Query Match Best Logal Similarity

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AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120
                       EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
                                                       TLVTVSSGGGGGGGGGGGGGG-SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK
                                                                                   Single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218..226
/note- "complementarity determining region 3"
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/note= "complementarity determining region
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 Indels
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/note- "heavy chain variable region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..163
te= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..195
te= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                               "complementarity determining
31;
                                                                                                                                                                                                                                             Anti-platelet glycoprotein Ib human scFv HIb-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "vector-derived linker"
                                                                                                                                                                                                                                                                                                                                                 "framework region 1"
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/note= "framework region 2"
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 Mismatches
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note
196..217
                                                                                                                                                                                               AAY95219 standard; Protein; 237 AA
26;
                                                                                                                                                                                                                              (first entry)
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 Conservative
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                                                                                                                                                                                                                                                                                           - Homo sapiens.
- synthetic.
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131. 23.
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                           249
                                                                                                                                                  FGGGTKLTVL
                                                                                                                                                                                                                              29-AUG-2000
181;
                                                                                                                                                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                              AAY95219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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(first entry)

10-NOV-1998

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The invention relates to antibodies specific to pectin, such as PAMI and PAM2 scFv (single chain variable region). These antibodies are derived from a naive phage display library known as the synthetic scFv Library (#1). PAMI and PAM2 antibodies are capable of binding to de-esterified and un-substituted homogalacturonan (HG), useful for identifying a pectin motif. PAM antibody is useful for identifying a pectin motif or can be used to prepare a food for human and animal consumption, such as jams, yogurts or gels. The PAM antibodies are further useful for quantifying the amount of pectin in a sample or for extracting pectin from a sample. PAM antibodies are also used to identify de-esterified homogalacturonan blocks in the primary cell walls of plants. The present sequence is PAM1 scFv antibody specific to pectin.

Note: This sequence is stated as being the same as that shown as sequence has 2 extra residues at the C-terminal end.
                                                                                                                                                                                                                                                                                     fying a pectin molety, for a sample or for extracting pectin
                                                                                                                                                                                                                                                                     of binding de-esterified
                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                     homogalacturonan, useful for identi
quantifying the amount of pectin in
from a sample
                                                                                                                                                                                     כי
                                                                                                                                                                                                                                                                   New PAM1 and PAM2 antibodies capabl
                                                                                                                                                                                 Mikkelsen
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 4B; 21pp; English.
                                                                                                                   98GB-0028700
                                                                                 99US-0260527
                                                                                                                                                                                   Willats WGT,
                                                                                                                                                                                                                WPI; 2001-342672/36.
N-PSDB; AAD06193.
                                                                                                                                                   (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 AA;
                US6228599-B1
                                                                             26-FEB-1999;
                                                                                                                 24-DEC-1998;
                                               08-MAY-2001
                                                                                                                                                                                    JP,
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                   Gaps
                                    GYYMYWVRQAPGQGLEWMGWINPNSGG--T 58
                                            NYAQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWG
                                                                                RGTLVTVSSGGGGGGGGGGGGGSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQ
                                                                                                                   KPGQAPVLV1YGKNNRPSG1PDRFSGSSSGNTASL11TGAQAEDEADYYCNSRDSSGNHV
                                                                                                                                                    13;
                   Indels
951.5; DB 22;
No. 8.4e-57;
smatches 29;
                   Mismatches
                                   EVOLVOSGAEVKKPGASVKVSCKASGYTFT
 Score
Pred.
                 25;
71.6%;
ilarity 73.3%;
Conservative 2
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Query Match
Best Local Similarity
                                                                                                                                                                             VEGGGTKLTVL
                                                                                                                                                                                       184;
                 Matches
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AAW49693 standard; Protein; 254 AA.

AAW49693 ID

AAW49693;

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This sequence represents a single chain antibody (ScFv4) constructed from the sequence encoding a human antibody raised against the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molety found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                             galactose;
                                                                        Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig; graft tissue rejection; organ transplantation; xenotransplant; human; single chain antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----awrtd-wgqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKFQGRVTMTRDTS1GTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLVTVSSGGGGTGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic non-human donors of organs for human recipients - containing DNA encoding antibodies that inhibit graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                             Human ScFv4 against alpha-1,3-galactosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 947.5; DB 19;
Pred. No. 1.4e-56;
7; Mismatches 29;
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llarity 72.3%;
Conservative 27
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Best Local Similarity
Matches 180; Conserv
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                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                Pourcel C,
                                                                                                                                                         Synthetic
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                     PAM1 single
                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2001
                                                                                                                                              Sequence
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            yogurt;
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Matches
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                                                                                                                                       DPAVSVALGQTVRITCQGDSLRSYYASWYQQKP 180
                                                              Gaps
                                                                             9
                                                                                                                                                                                                                                                                                                                      Apo-2; receptor; apoptosis; neurodegenerative disease; cancer; necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
      designated 16E2
                                                                         YTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
                                                                                  SDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
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:aedtavyycakilgag----rg-wyfdlwgkg
                                                                                                                                            and produce
                                                            9
                                             309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to treat
                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis - useful to tapoptosis e.g. cancer, e apoptosis
     antibody,
                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.C.
                                           ; DB 20;
7.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim
                                                          Mismatches
     ain Apo-2
                                         ore 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               rapai A,
                                           Scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Apo-2 polypeptide inducing ap conditions linked with decreased ap antibodies to increase or decrease
                                                                                                     AQKFQGRVTMTRDTSIGTAYMELSRLS
                                                                                                              | :||||::|| : : |:::: | adsvkgrvtisrdnaknslylgmnslr
                                                                                                                                    TLVTVSSGGGGGGGGGGSSELTC
                                                                                                                                                                  GOAPVLVIYGKNNRPSGIPDRFSGSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chuntha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Fig 16; 134pp; Englis]
     G
                                                                      1 EVQLVQSGAEVKKPGASVKVSCKASG)
                                                                                 evqlvqsgggverpggslrlscaasg
                                                                                                                                                                                                                                                                                                      Single chain Apo-2 antibody 20E6
                                                                                                                                                                                                                                                       AAW83323 standard; Protein; 312
                                       75.0%; Scilarity 76.3%; Pl
Conservative 24;
   single
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0020746
97US-0857216
                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US09704
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
  sequence represents
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-045228/04.
N-PSDB; AAV72533.
                  A.
                                                                                                                                                                                                   249
                                                                                                                                                                                                  GGGTKLTVL : | GGGTKLTVL : | GGGTKltvl : |
                                                                                                                                                                                                                                                                                                                       Apo-2;
                                                                                                                                                                                                                                                                                                                               tumour necro
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   WO9851793-A1
                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1998;
15-MAY-1997;
                                                                                                                                                                                                                                                                                       16-MAR-1999
                                                       190;
                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1998
                 Sequence
                                       Query Match
Best:Local
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                                                                                                                                                                                                                                                                        AAW83323;
                                                                                                                                                                                                                                                                                                                      Human;
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                                                      Matches
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binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope activation allow Apo-2 detection and purification using anti-tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially mammalian cancer cells, and antagonistic antibodies used to block antibodies may also be used diagnostically e.g. to detect Apo-2 expression in cells/tissues and in Apo-2 purification. The present sequence represents a single chain Apo-2 antibody, designated 20E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scFv; food; jam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 QKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARD--RYYGSSAYHRGSYYMDVWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTLVTVSSGGGGTGGGGGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single chain variable region;
curonan; HG; plant cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 963.5; DB 20;
Pred. No. 1.4e-57;
26; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain variable region (scFv) antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label* pelB_leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23..140 -
/label- Heavy_chain_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157..277
/label= Light_chain_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277..282
/note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267..277
/label Myc_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     V Match
Local Similarity 73.6%; Pr
hes 184; Conservative 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; single chomogalacturonan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141..156
/label= Linker
157..277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                                           312 AA;
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aqkfqgrvtmtrdtsistaymelsslrsedtavyyca-
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                                                                                                                                                                     AAW83322 standard; Protein; 309 AA.
                                                                                                                                                                                                                               Single chain Apo-2 antibody 16E2
                    GTLVTVSSGGGGGGGGGGGSS---
                                                                                                                                                                                                                                                                                                                                                    98WO-US09704
                                                                                                                                                                                                                                                                                                                                                                       98US-0020746
97US-0857216
                                                                                                                                                                                                            (first entry)
                                                                                                 SGNHVVFGGGTKLTVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi AJ,
                                                                                                          t-dlivfgggtkltvl
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N-PSDB; AAV72532.
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                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                        AAW83322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in antibody (scFv) fragments which antigen (HLA)-Cw6. The fragments are ombinatorial antibody library based on nd CDRs randomised with trinucleotides. man immunoglobulin fragments specific e is considered highly relevant in ilencing as well as miscarriages. brium in some recurrent abortions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-Cw6. The anti-HLA-Cw6 immunoglobulin ration of a pharmaceutical for the useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; HLA; HLA-Cw6; natural killer cell silencing; ortion; psoriasis; antibody; HLA phenotyping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                                                                                                            ic scFv fragment from clone Cw6_3.
                                                GSSAYHRGSYYMDVWGRGTLVTVSSGGGGTG
                                       IQGDSLRSYYASWYQQKPGQAPVLVIYGKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----wgqgtlvtvsrggggsg
                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 245;
                                                                            EADYYCNSRDSSGNHVVFGGGTKLTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 1011.5; DB
NO. 6.6e-61;
21;
                                                                                                                                                                                                                                                                                                                                                                                  Kroenke M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB67617-23 represent single chain ant are specific for human leukocyte antig derived from a synthetic human combina molecular consensus frameworks and CDR The specification describes a human im for HLA-CW6. The HLA-CW6 serotype is c studies of natural killer cell silenci HLA-CW6 demonstrates a disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 11arity 77.0%; Pred. Conservative 19; Mis
                                                                            Psoriasis may also be linked to His
fragments are useful for the prepartreatment of humans. They are also
                                                                                                                                                                                                            Human leukocyte antigen-Cw6 specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSIGTAYMELSRLSSDDTAVYYCARDRYY
          || ||||||||| | |:||||||||| | tsastaymelsslrsedtavyycarsgvy
                                       GGGSGGGSSELTQDPAVSVALGQTVRIT
                                                                                                                                                  245 AA
                                                                                                                                                                                                                                           miscarriage; abortion; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                   Marget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1; 23pp; English
                                                                                                                                                AAB67619 standard; Protein;
                                                                                                                                                                                                                                                                                                                        2000WO-EP08388
                                                                                                                                                                                                                                                                                                                                          99EP-0116691
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 AA;
                                                                                                                                                                                                                              Human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                 Ė
                                                                                                                                                                                                                                                                                WO200114558-A1
                                                                                                                                                                                                                                                                                                                        28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                          26-AUG-1999;
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                Kretzschmar
                                                                                                                                                                                        29-MAY-2001
                                                                                                                                                                                                                                                                                                    01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197;
                                                                                                                                                                     AAB67619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local
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                                                         107
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                  61
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The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer.

Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNF). The cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be therapeutically (e.g. those containing immunoglobulin sequences can be complicated allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies which capptosis in mammalian cancer cells, and antagonistic antibodies used to block excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2 extression in cells/tissues and in Apo-2 purification. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
TNFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis
-rgsfdfmdnwgg
                                                                                       --ELTQDPAVSVALGQTVRITCQGDSLRSYYA
                                                                                                                                                                                                                                                                               SWYOOKPGOAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDS
                                                                                                                                                                                                                                                                                                                            Human; Apo-2; receptor; apoptosis; neurodegenerative disease;
tumour necrosis factor; TNF; tumour necrosis factor receptor;
TNF cytokine.
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230 gggtkltvl

В

232

FGGGTKLTVL

240

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used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the anti-murine CTLA-4 sFv (M19 sFv). This is a membrane-associated protein which binds to CTLA-4. Chimeric constructs comprising DNA sequences encoding the extracellular domain of murine CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein. The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated T-cells and antagonises the co-stimulatory signal provided by the interaction between donor B7 and recipient CD28. Cells expressing the anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
                                                                                                                     # sle chain antibody; murine CTLA4;
construct; extracellular domain;
co-stimulatory signal; donor B7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of xenotransplanted organs
                                                                                                                                                                                                                                                                    atc codon"
                                                                                                                                                                                                                                                                                                                                                                                                  IONS LTD.
                                                                                                                                                                                                                                                           /note= "Corresponds to
                                                                                                               Anti-murine CTLA-4 sFv; M19 sFv; singl membrane-associated protein; chimeric human CD8; ligand; activated T-cell; crecipient CD28; T-cell proliferation; xenograft-specific immunosuppression.
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                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-cells and antagonises the co-st
interaction between donor B7 and
anti-hCTLA4 sFv failed to stimula
xenograft-specific immunosuppress
                                                                                                                                                                                                                                                                                                                                                                                           (IMCO-) IMPERIAL COLLEGE INNOVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting T-cell mediated reject
                242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
               Protein;
                                                                                                                                                                                                                                                                                                                                                                     98GB-0009280.
                                                                                                                                                                                                                                                                                                                                           99WO-GB01350
                                                                                          SFV
                                                                (first entry)
                                                                                        Anti-murine CTLA-4 M19
                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 11; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                       Dorling
                                                                                                                                                                                                                                   Key
Misc-difference 208
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038815/03
N-PSDB; AAZ28999.
               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 AA;
                                                               07-FEB-2000
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                                                                                                                                                                                                                                                                                                                                        30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                  30-APR-1998;
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                                                                                                                                                                                               Mus sp.
Synthetic.
             AAY15127
                                      AAY15127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Lechler
                                                                                                                                                                                             Mus
AAY15127
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This sequence represents a single chain antibody (ScFv5) constructed from the sequence encoding a human antibody raised against the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molety found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ή
                                                                                                                                                                    galactose;
                                                                                                                                                          Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose
sugar; N-acetyllactosamine; glycoproteln; glycolipid; antibody; pig;
graft tissue rejection; organ transplantation; xenotransplant; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic non-human donors of organs for human recipients -containing DNA encoding antibodies that inhibit graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                         Human ScFv5 against alpha-1,3-galactosyl transferase.
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Pred. No. 1.3e-63;
'; Mismatches 15;
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                               standard; Protein; 229 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 56-57; 71pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                          (INRM ) INSERM INST NAT SANTE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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Best Local Similarity 84.7%;
Matches 200; Conservative 7
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soulillou JP,
                                                                                                                                                                                                           single chain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-112876/11.
PB; AAV49461.
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                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                            10-NOV-1998
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                                                               AAW49694;
                             AAW49694
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L.9e-64;

ore 1064; D red. No. 1.9e Mismatches

Scor

Query Match
Best Local Similarity 83.6%;
Matches 209; Conservative 1

11;

Length 242;

FTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY

AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120

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EVQLVQSGAEVKKPGASVKVSCKASGYT

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AAW49692;

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This sequence represents a single chain antibody (ScFv2) constructed from the sequence encoding a human antibody raised against the porcine enzyme the sequence encoding a human antibody raised against the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a plg, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
 rotein; glycolipid; antibody; pig;
splantation; xenotransplant; human;
                                                                                                                                                                                                                                                                                                                                                                      recipients -
graft rejection
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inhibit
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sugar; N-acetyllactosamine; glycop;
graft tissue rejection; organ trans
single chain antibody.
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                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV49458
                                                                                                                FR2751346-A1
                                                                                   Homo sapiens
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ä AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG 120 107 Gaps 9 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY ----idqwgqg DB 19; Length 237; 13; Indels e 1073.5; DB 19; No. 4.2e-65; ismatches 20; Score Pred. GQAPVLVIYGKNNRPSGIPDRFSGSSSGW gapvlviygknnrpsgipdrfsgssgn .. B 80.8%; |larity 83.5%; |Conservative 6 Query Match Best Local Similarity Matches 208; Conser GGGTKLTVL 249 61 168 228 -121 108 241 181 61 셤 õ õ 음 ô ద õ ð 셤

AAW49692 standard; Protein; 239 AA

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RESULT

AAW49692

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This sequence represents a single chain antibody (ScFv3) constructed from the sequence encoding a human antibody raised against the porcine enzyme alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants. Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
                                                                                      galactose;
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                                                                               Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig; graft tissue rejection; organ transplantation; xenotransplant; human; single chain antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic non-human donors of organs for human recipients -
containing DNA encoding antibodies that inhibit graft rejection
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                                                       Human ScFv3 against alpha-1,3-galactosyl transferase
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81.5%; Pred. No. 1.7e-64;
ive 12; Mismatches 23;
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N-PSDB; AAV49459.
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Matches 203; Conserv
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Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
  FR2751346-A1
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                                                                                                     receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor antibody can be used as an agonist of a cell expressing the WSX receptor. It can also differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, cspecially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to reappulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and cholelithiasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactose;
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                         and ligands - used e.g. for improving
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                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1329; DB 18
100.0%; Pred. No. 2.7e-82;
tive 0; Mismatches 0;
                                                                         English
                       WSX receptor and related antibodies and products for diagnosis and therapy, e.g haematopoiesis or for treating tumours
                                                                                                agonist
                                                                        Example 14; Pages 120-121; 219pp;
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Best Local Similarity 100.
Matches 249; Conservative
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WPI; 1997-372864/34
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Homo sapiens
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This sequence represents a single chain antibody (ScFv1) constructed from the sequence encoding a human antibody raised against the porcine enzyme talpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses the attachment of a galactose sugar molecule on the N-acetyllactosamine molety found on surface glycoproteins and glycolipids. These sugar molecules are partly responsible for raising anti-graft antibodies, which lead to graft tissue rejection. The invention relates to a method of inhibiting the graft rejection mechanism by introducing the sequence encoding an antibody targeted to alpha-1,3-GT into the cells of animal, especially a pig, from whom organs may be used for xenotransplants.

Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking the galactose on the glycoproteins and glycolipids, thus preventing induction of the rejection response.
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graft rejection
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Pred. No. 3.7e-67;
9; Mismatches 15;
                                                                                                                                                                                                                                                                                   or human
inhibit
                                                                                                   RECH MEDICALE
                                                                                                                                                                                                                                                                                   Transgenic non-human donors of organs for containing DNA encoding antibodies that in
                                                                                                                                                      Vanhove B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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84.78;
96FR-0009077
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hes 211; Conservative
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N-PSDB; AAV49457.
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| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
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| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
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| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
| SibSi/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
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Anti-murine CTLA-4
Human SCFv5 agains
Human leukocyte an
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Single chain Apo-2
PAM1 single chain
Human ScFv4 agains
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ScFv2 agains
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Maximum Match 100%
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AAW49691
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AAB46052	519	605	197	AAB67617	505	5	AAE02186	22	22	762	508	90	22	363	53	348		258	2	102	548	175	258	348	88	5648	356		258	48	AAR22585	œ
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## ALIGNMENTS

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Human; WSX receptor; clone #3; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
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                                                                                      Human WSX receptor agonist antibody clone
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                   249
                     standard; Protein;
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96US-0585005
                                                                                                                                                                                                                                                                        97WO-US00325
                                                                (first entry)
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Rodrigues ML;
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08-JAN-1996;
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                                          AAW24061;
                   AAW24061
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         AAW24061
RESULT
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15;

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Length Indels

DB 2;

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FINUSOL 19 heavy chain v region (G6+ T-L42) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C; Accession: PH0962
R; Martin, T; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies.
A; Reference number: PH0952; MUID:92202880
A; Reference number: PH0952; MUID:92202880
A; Ratus: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-120 < MAR>
C; Superfamily: immunoglobulin v region; immunoglobulin
B; 1-30/Region: immunoglobulin homology < C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < CiMM>
F; 15-98/Domain: immunoglobulin homology < CiMM>
F; 31-35/Region: complementarity-determining 1
F; 36-50/Region: complementarity-determining 3
F; 99-108/Region: complementarity-determining 3
F; 99-108/Region: complementarity-determining 3
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                                                                                                                                                                                                                                                                           EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
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Pred. No. 1.7e-26;
; Mismatches 12;
                                                     Score 504.5; DB 2
Pred. No. 1.5e-26;
}; Mismatches B
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76.7%;
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Local Similarity 80.0%;
hes 100; Conservative
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                                                                                    Local Similarity
hes 102; Conser
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A; Accession:

A; Molecule type: protein

A; Residues: 1-111 cGAR>
C; Comment: The sequence of the variable region only is shown.
C; Comment: This is a Bence Jones protein.
C; Comment: This is a Bence Jones protein.
C; Comment: This is a Bence Jones protein.
C; Complex:
C; Compl
                                                                                                                                                                                                                                                                                                                                                                                                       Ig lambda chain V-II region (Nei) - human

C;Species: Homo sapiens (man)

C;Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999

C;Accession: A01970

R;Garver, F.A.; Hilschmann, N.

Eur. J. Biochem. 26, 10-32, 1972

A;Title: The primary structure of a monoclonal human lambda-type immunoglobulin L-chain
A;Reference number: A01970; MUID:7223323
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                                                                                                                                     61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYYYMDVWGKG
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRV - - VVPATSLRGGMDVWGQG
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ed. No. 1.1e-26;
Mismatches B;
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llarity 87.3%; Pred.
Conservative 6; Mis
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Ig heavy chain V-1 region (AND) - human
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Best Local S
Matches 96
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C; Accession: PH0955
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies.
A; Reference number: PH0952; MUID:92202880
A; Reference number: PH0952; MUID:92202880
A; Reference number: PH0952; MUID:92202880
A; Reference number: PH0955
A; Reference number: PH0955
A; Reference number: PH0952; MUID:92202880
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-30/Region: framework 1
F; 15-98/Domain: immunoglobulin homology <IMM>F; 15-98/Domain: immunoglobulin homology <IMM>F; 15-98/Domain: framework 1
F; 36-50/Region: complementarity-determining 2
F; 51-67/Region: complementarity-determining 2
F; 51-67/Region: complementarity-determining 2
                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0957
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0957
A;Accession: PH0957
A;Accession: PH0957
A;Accession: PH0957
A;Accession: PH0957
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>F;1-30/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: framework 3
F;99-113/Region: complementarity-determining 3
F;99-113/Region: complementarity-determining 3
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Pred. No. 4.3e-27;
8; Mismatches 17
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Pred. No. 7.9e-27;
9; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;68-98/Region: framework s
F;99-115/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PH0955
Ig heavy chain V region (G6+ CLL-AND)
                                                                                                      Ig heavy chain V region (G6+ CLL-BRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.2%;
llarity 80.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G.; Hamblin, T.J.; Stevenson, F.K.
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C. Dapecles: Homo sapiens (man)
C. Dapecles: Homo sapiens (man)
C. Dan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C. Accession: S44105
R. Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K submitted to the EMBL Data Library, March 1994
A. Description: Idiotypic vaccination against human B-cell lymphoma: rescue of v A; Reference number: S44105
A. Accession: S44105
A. Accession: S44105
A. Accession: S44105
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-112 < HAW>
A. Residues: 1-112 < HAW>
A. Residues: BMBL: Z31388; NID: g472959; PIDN: CAA83263.1; PID: g940517
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology < IMM>
b.
                                                                                                    17-Apr-1993 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY
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                                                                                                                                                                              of natural autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCSSYTTRSTR-VFGGGTKLTVL 250
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ulin
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YCSSYTSSSTRYVFGTGTKVTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
10; Indels
                                                      human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.5%; Score 513.5; DB 2; ilarity 91.0%; Pred. No. 3.5e-27; Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 517; DB 2;
Pred. No. 2.2e-27;
7; Mismatches 10
                                                                                                                                                   ; Kipps, T.J
                                     Ig heavy chain V region (G6+ T-L33) - human (fra C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-19
C; Accession: PH0961
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natur A; Reference number: PH0952; MUID:92202880
A; Accession: PH0961
A; Satus: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-119 < MAR>
C; Superfamily: immunoglobulin V region; immunogl C; Keywords: heterotetramer; immunoglobulin F; 1-30/Region: framework 1
F; 36-50/Region: complementarity-determining 1
F; 56-50/Region: complementarity-determining 2
F; 68-98/Region: framework 3
F; 99-107/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTITADESTSTAYMELSSLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 SNRFSGSKSGSTASLTISGLQAEDEADY
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Best Local Similarity 81.6%;
Matches 102; Conservative
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Best Local Similarity
Matches 101; Conserv
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17-Apr-1993 #text_change 16-Aug-1996
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C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16..
C:Accession: PH0954
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
C;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: framework 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 3
F;99-120/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                       Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 132;
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                                                                          immunoglobulin homology
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PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
                                                                                                                                                                                                                                                                                                                  i; DB 2;
..6e-27;
les 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 518.5; DB 2;
Pred. No. 2e-27;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                     Score 519.5;
Pred. No. 1.6e
7; Mismatches
                       A; Molecule type: DNA
A; Residues: 1-122 < MAR>
C; Superfamily: immunoglobulin V region; immunogloc; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 1-30/Region: framework 1
F; 31-35/Region: complementarity-determining 1
F; 36-50/Region: framework 2
F; 51-67/Region: complementarity-determining 2
F; 68-98/Region: framework 3
F; 99-110/Region: complementarity-determining 3
         nucleic acid sequence not shown
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Similarity 75.9%;
34; Conservative 8
                                                                                                                                                                                                                                                                                                                       40.0%;
llarity 82.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 YYGMDVWGOGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTVSS 125
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Best Local Sim
Matches 104;
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R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A; Title: Developmentally restricted immunoglobulin heavy chain variable region gene
A; Reference number: A33548; MUID:89345575
A; Accession: C.33548
A; Accession: C.33548
A; Accession: C.33548
A; Reference number: A33548; MUID:89345575
A; Accession: C.33548
A; Reference number: A33548; MuiD:89345575
A; Accession: C.33548
A; Reference number: A33548; MuiD:89345575
A; Residues: 1-133 <KIP>
A; Residues: 1-133 <KIP>
A; Experimental source: the sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C; Accession: PH0958
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies.
A; Reference number: PH0952; MUID:92202880
A; Accession: PH0958
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                                                                                                                                                                               526.5; DB 2;
No. 6.1e-28;
smatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core 524; DB 2;
red. No. 8.7e-28;
Mismatches 11
                                                                                                                                                                                                                                 Mismatches
F;15-98/Domain: immunoglobulin homology <IMM F;31-35/Region: complementarity-determining F;36-50/Region: framework 2 F;51-67/Region: complementarity-determining F;58-98/Region: framework 3 F;99-124/Region: complementarity-determining
                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                           EVQLVQSGAEVKKPGESLKISCQGSGFTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 77.4%; Pred.
Matches 103; Conservative 11; Mis
                                                                                                                                                                                                                                10;
                                                                                                                                                                                 40.5%;
nilarity 76.5%;
Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YGMDVWGQGTTVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 -GMDVWGQGTTVTVSS 125
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                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 104; Conserv
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SYTTRSTRVFG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GGGGSGGGGSGGGSQSVLTQ-PASVSGSPGQSITISCTGTSS-DVGGYNYVSWYQQHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 KAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSY--TTRSTRVF
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                                                                                                                                                                           ASVSGSPGQSITISCTGTSSDV--GGYNYVSW
                                                                                                                                                                                                                                                                                    178 YQQHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRS
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GSGSGTSFTLRISRVEAEDVGVYYCMQH-REY
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                                                                                                           Length
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                                                                                               628; DB 2; Le
No. 2.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a single-chain
950
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ed. No. 6.5e-32;
Mismatches 69;
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                                                                                                        Query Match
Best Local Similarity 52.4%; Pred.
Matches 131; Conservative 36; Mi
                                                                                                                                                             1 EVQLVQSGAEVKKPGESLKISCQGSGFT
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                                                                                                                                                                                                                                                                                    61 AQKFQGRVTITADESTSTAYMELSSLRS
                                                                                                                                                                                                                               61 VPRFQDKATITADTSSNTAYLLLSSLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
A; Reference number: S41374
A; Accession: S41374
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-249 <ART>
A; Cross-references: EMBL: Z29480
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234 PLTFGAGTKL 243
                                                                                                                                                                                                                                                                                                                                                                              238 TRVFGGGTKL 247
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Best Local Simi
Matches 127;
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PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C; Accession: PH0960
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies.
A; Reference number: PH0952; MUID:92202880
A; Accession: PH0960
A; Accession: PH0960
A; Accession: PH0960
A; Accession: L136 < MAR>
C; Superfamily: inmunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                       23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATS-----LRGGM 112
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                                                                                                                                                                                                                                                                                                                 PID:933451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EGSKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --0HPG--
                 C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: S14683; S08047
R; Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

R; Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990
A; Title: Complete nucleotide sequence of the membrane form of the h
A; Reference number: S14683; MUID:90332450
A; Reference number: S14683; MUID:90332450
A; Residues: 1-627 <FRI>
A; Residues: 1-627 <FRI>
A; Residues: 1-627 <FRI>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin; membrane protein
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 16-627/Product: Ig mu chain #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627;
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36.9%; Pred. No. 5.7e-28;
ive 27; Mismatches 68
membrane-bound (cloné 201)
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Best Local Similarity 36.9
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2000
 GenCore ver
Copyright (c) 1993 - 2
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- protein search, using sw model OM protein Search time 54.95 Seconds (without alignments) 437.167 Million cell updates/sec --01 August 15, 2002, 16:25: Run on:

US-08-779-457-49 1300 Title: Perfect score: Sequence:

....SSYTTRSTRVFGGGTKLTVL 250 1 EVQLVQSGAEVKKPGESLKI.

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

esidues 283138 seqs, 96089334 r Searched:

283138 arameters: Total number of hits satisfying chosen p

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summar

tes

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

	Description	Ig heavy chain V r	single chain Fv an	p53 specific singl	g mu chain p	g heavy cha	. 67	_ 	g heavy	 	g lambda	g heavy c	57	g lambda	g heavy c	Ig heavy chain V r	g lambda	<b>.</b>	ь	_ _	Ig lambda chain V	<u>ب</u>	Ig heavy chain V r	r in	Ig lambda chain V	Iq lambda chain V	Iq heavy chain V r	Ig lambda chain -	Ig lambda chain V	Ig heavy chain pre
SUMMARIES	ID	A56446	S41374	JC5322	S14683	PH0960	C33548	PH0958	PH0954	PH0961	S44105	PH0957	PH0955	LZHUNI	B33548	PH0962	S44123	S46394	A33548	S31515	S36281	PH0959	PH0952	L2HUNG	S46395	S46396	PH0953	S25758	S36256	B32274
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	Score	648.5	628	591	537.5	526.5	524	519.5	518.5	517	513.5	513	503	506	504.5	503.5	501.5	501.5	200	498.5	497	496.5	496.5	94.	•	σ	Q.	8	4	481.5
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3366123356678889000000000000000000000000000000000	35.4 8.8
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### ALIGNMENTS

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A; Reference number: A56446; MUID:95229583

A; Reference number: A56446

A; Reference number: A56446; MUID:95229583

A; Reference number: A56446

A; Residues: 1-268 < TAN>

A; Residues: I-268 < TAN < TA
RESULT
A56446
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Gaps 13; Length 268; Indels Query Match 49.9%; Score 648.5; DB 2; Best Local Similarity 53.6%; Pred. No. 1.3e-35; Matches 134; Conservative 33; Mismatches 70;

4

115 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120 OHPGKAPKLMIYEGSKRPSGVSNRFSGSKSGSTASLTISGLQAEDEADYYCSSYTTRSTR 239 60 62 OKSDASPKLWYYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATXYCQQFTS-SPF 1 EVQLVQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY 180 172 d ò g 吕 d Q ò ò

240 VFGGGTKLTV 249 ð

RESULT 2
S41374
single chain Fv antibody - mouse
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C; Accession: S41374
R; Artsaenko, 0.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A; Description: Construction and functional characterization of a single chain Fv anti

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                                                                                            Length 673;
                                                                                             Query Match 54.4%; Score 723.5; DB 4; Best Local Similarity 55.1%; Pred. No. 4.4e-52; Matches 141; Conservative 44; Mismatches 54;
                                                        NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO
US-09-423-439-32
                                                                                                                                                                                                                                                                                              251 QSYTLRTEGGGTKLEI 266
                                                                                                                                                                                                                                                                                    233 SSGNHVVFGGGTKLTV 248
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Search completed: August 15, 2002, 16:22:14 Job time: 424 sec

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RESULT 15
US-09-423-439-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 244;
                                                                                                                                                                                                                                                                                                                                               Score 727.5; DB;
Pred. No. 6.2e-53,
31; Mismatches 64
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Patent No. 6339070
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123,439
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,4:
FILING DATE: 09-NO. 6339070-1999
 PCT/EP95/00978
                                                                                                                                                             26
                                                                                 APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1.726
TELEPHONE: 703-243-6333
TELEPHONE: 703-243-6333
INFORMATION FOR SEQ ID NO: 20:
                                   JA-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pillsbury Winthr STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 KPGSSPRLLIYDTSNLASGVPVRFSGSGSG
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.4%; Pred.
Matches 146; Conservative 31; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AOKFOGRVTMTRDTSIGTAYMELSRLSSDD
APPLICATION NUMBER: WO PORTING DATE: 16-MAR-1995
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COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                              : 244 amino acids
amino acid
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
            FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: E
                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-553-497A-20
                                                                    PRIOR APPLICATION DATA:
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234 TFGGGTKLEI 243
                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                Length 288
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                                                                                                                                                                                                                                                                                                                                                            Query Match 54.4%; Score 723.5; DB 4; Best Local Similarity 55.1%; Pred. No. 1.6e-52; Matches 141; Conservative 44; Mismatches 54;
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.I
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA
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US-08-553-497A-20
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                                                                                                                            & HAND,
                                                                                                                                                                                                                                                   Version #1.25
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.4e-55;
es 53;
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No. 3.4e
|smatches
                                                                                                                           ERG KIEL
                              GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for ta
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
                                                                                                                                                                        COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 74, Application US/08918148A Patent No. 6342220 GENERAL INFORMATION: APPLICANT: Adams, Camellia APPLICANT: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%; Score
60.1%; Pred.
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| CERPDHLFTGLIGGTNNRAPGVPARFSGS
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                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
US-08-491-988-5; Sequence 5, Application US/08491988; Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-810
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TWOTH: 435 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-491-988-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 HVVFGGGTKLTVL 249
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Best Local Similarity
Matches 152; Conser
                                                                                                                                                                                                                                                                                        FILING DATE:
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US-08-918-148-74
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                                                                                                                                                                                                                                                        Length 249;
                                                                                                                                                                                                                                                                                             Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                        Score 736.5; DB 4;
Pred. No. 1.2e-53;
40; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, STREET: 2200 CLARENDON BLVD. SUITE 1400 CITY: ARLINGTON STATE: VA
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 74
LENGTH: 249
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08553497A Patent No. 5844093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KETTLEBOROUGH, C. A. APPLICANT: BENDIG, MARY M. APPLICANT: ANSELL, KEITH H. APPLICANT: GUSSOW, DETLEF APPLICANT: ADAN, JAUME APPLICANT: MITJANS, FRANSESC APPLICANT: ROSELL, ELISABET APPLICANT: BLASCO, FRANCESC APPLICANT: PIULATS, JAUME TITLE OF INVENTION: ANTIBODIES MINNED OF SECURATES.
                                                                                                                                                                                                                                                                                             40;
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ilarity 57.3%;
Conservative 4
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APPLICATION NUMBER: US/CFILING DATE: 17-NOV-1995
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 HVVFGGGTKLTVL 249
                                                                                                                                                                                  ; ORGANISM: artificial US-08-918-148-74
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 145; Conserv
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   AVSVALGQTVRITCQ --- GDSLRSYYASWY 176
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1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSS-----YFDYWGQG
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les 53;
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ed. No. 3.1e
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                       APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for tal
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG
STREET: 261 MADISON AVENUE
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60.1%; Pred. N
ative 35; Mism
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                                                                                                                                                                                       Sequence 9, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-918-9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy At
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                               GENERAL INFORMATION
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US-08-491-988-9
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Best Local Sim
Matches 152;
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
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                                                                                                                                                                  APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Ven
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELEPHONE: 212-986-4090
TELEPHONE: 212-986-4090
TELEPHONE: 212-986-4090
                                                                                                                   Sequence 7, Application US/08491988 Patent No. 5973116 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
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HVVFGGGTKLTVL 249
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Matches 152; Conser
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STREET:
CITY: NE
STATE: N
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US-08-491-988-3
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No. 1.9e-55;
ismatches 53;
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les 57;
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. No. 4.1e
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07/05/95
NN: 514
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Pred.
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Pred.
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APPLICANT: Spooner, Robert A. APPLICANT: Epenetos, A.A.
                                                                                                                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                            40 QVQLVQSGGGVVQPGRSLRLSCAASGFIF
                                                                                                                                                                                                                                                                                                                                                                                                                AQKFQGRVTMTRDTSIGTAYMELSRLSSD
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60.1%;
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60.5%;
                        INFORMATION FOR SEO ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
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Best Local Similarity 60.1
Matches, 152; Conservative
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    650/952-9881
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FILING DATE: 07/05,
CLASSIFICATION: 51
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Best Local Similarity
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; MOLECULE TYPE:
US-08-428-257A-72
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                                                                                                   TYPE: Am TOPOLOGY:
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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                                                                                                                                     AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
                                                                   TLVTVSSGGGGTGGGGGGGGGS-SELTQDPAVSVALGQTVRITCQ---GDSLRSYYASWY
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ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND,
STREET: 261 MADISON AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e-55;
ches 53;
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18-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: EPENETOS, AGAMEMNON A. APPLICANT: SPOONER, ROBERT A. APPLICANT: DEONARAIN, MAHENDRA TITLE OF INVENTION: Compounds for NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08491988 Patent No. 5973116 GENERAL INFORMATION:
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NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                            254 HWVFGGGTKLTVL 266
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                                                                                                                                                                                                                                                            HVVFGGGTKLTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 152; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino addition; TOPOLOGY: line; MOLECULE TYPE: 1
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4

1 EVQLVQJGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY

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-779-457-48

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SPSFQGQVTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKWPEYFQHWG
                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARD--RYYGSSAYHRGSYYMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGTLVTVSSGGGGGGGGGGGGGGGGG-SELTQDPAVSVALGQTVRITCQGDS--LRSYYASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 YQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG
                                                                                                                                                                                                                                                                                                                                                                  EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWYRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                        Score 776.5; DB
Pred. No. 6e-57;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09079029; Sequence 11, Application US/09079029; Patent No. 6342369; GENERAL INFORMATION:
APPLICANT: Adams, Camilia W. APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us/09/079,029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,02
NAME: Hunter, 10000

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                        Ouery Match 58.4%; So
Best Local Similarity 60.2%; Pr
Matches 153; Conservative 35;
                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGWVFGGGTKLTVL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 NHVVFGGGTKLTVL 249
                                                                                                                                                                                           ; TOPOLOGY: 11
; MOLECULE TYPE:
US-08-665-202-5
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TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ITP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-homogalacturonan specific antibodies selected
from a naive phage display library known as the
Synthetic scFv Library (#1) from the Centre for
Protein Engineering, MRC Centre, Cambridge, UK
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMY-WVRQAPGQGLEWMGWINPNSGGTN 59
                                                                                                                                                                                                                                                                                                                                                                                       YAQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                         Length 278;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                        Score 884.5; DB 4;
Pred. No. 7.9e-66;
24; Mismatches 37;
      CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLVTVSRGGGGGGGGGGGGSSELTQDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 PGQAPVLVIYGKNNRPSGIPDRFSGSSSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTLVTVSSGGGGTGGGGSGGGSSELTQDP
                                                                                                                                                                                                                                                                                     66.6%; Score
llarity 70.4%; Pred.
Conservative 24; Mis
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US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marks, James D. APPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: A
OTHER INFORMATION: S
OTHER INFORMATION: S
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Best Local Similarity
Matches 176; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                SEQ ID NO 3
LENGTH: 278
                                                                                                                                                                                                                                  US-09-260-527-3
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23 EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHV
EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-homogalacturonan specific antibodies fro phage display library known as the Synthetic Library (#1) from the Centre for Protein Engineering, MRC Centre, Cambridge, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 2.4e-71;
; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOU19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
                                                                                                                                                                                                 Sequence 1, Application US/09260527A; Sequence 1, Application US/09260527A; Patent No. 6228599; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mikelsen, J.D.
TILE OF INVENTION: ANTIBODY
FILE REFERENCE: DYOU19.001AUS
CURRENT APPLICATION NUMBER: US/09/260,527A; CURRENT FILING DATE: 1999-02-26; NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.6%;
Best Local Similarity 73.3%;
Matches 184; Conservative 25
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: P
; OTHER INFORMATION: L
; OTHER INFORMATION: L
; OTHER INFORMATION: E
US-09-260-527-1
                                                                                              249
                                                                                                              240 FGGGTKLTVL
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US-09-260-527-1
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                                                                                                                            ----RG-WYFDLWGKG
                                                                AVSVALGQTVRITCQGDSLRSYYASWYQQKP
                                                                                61 AQKFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
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Pred. No. 2.7e-72;
26; Mismatches 33;
                    floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELEPHONE: 650/225-5416
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
COMMESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/079,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb is COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.5%; Score Best Local Similarity 73.6%; Pred. Matches 184; Conservative 26; Mi
                                                                                 TLVTVSSGGGGGGGGGGSSELTQDP
                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09079029 Patent No. 6342369
                                                                                                                                                                                                                                                                                                                                                                                                                                                Jenentech, Inc.
CITY: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 312 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                  Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams,
                                                                                                                                                                                                         274 GGGTKLTVL 282
                                                                                                                                                                                          GGGTKLTVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94080
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TOPOLOGY:
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                                                                                                                                                                                                                                                                     RESULT 2
US-09-079-029-10
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# Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 2000 Com

del SW IIIO - protein search, using OM protein

Search time 39.61 Seconds (without alignments) 153.546 Million cell updates/sec August 15, 2002, 16:22:13; Run on:

.....SRDSSGNHVVFGGGTKLTVL 249 US-08-779-457-48 1329 1 EVQLVQSGAEVKKPGASVKV. Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

231628 Total number of hits satisfying chosen parameters:

231628 segs, 24425594 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summari

ies

Database

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/FCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|     |          | de (           |        |             |                    |                   |
|-----|----------|----------------|--------|-------------|--------------------|-------------------|
| NO. | Score    | Query<br>Match | Length | DB          | QI                 | Description       |
| -   | 997      | ٠ -            | 309    | 4           |                    | Sequence 9, Appli |
| 7   | CT.      | α.             | 312    | 4           | -019-              | 10,               |
| m   | 2        | ä              | 280    | 4           | -09-260-527        | 1,                |
| 7   | 8        | 9,99           | 278    | 4           | -09-260-52         | Sequence 3, Appli |
| S   | w        | ъ.             | 258    | 7           | 'n                 | ິດ                |
| 9   | 67       | 7              | 310    | 4           | -019-              | 11                |
| 7   | 58       | ζ.             | 269    | 7           | -08-428-           | Sequence 72, Appl |
| 8   | 5        | _              | 269    | 7           | -98                | 3                 |
| σ   | S        | 7              | 402    | ď           | -08-491-           | 6                 |
| 10  | 58       | 57.1           | 415    | 2           | US-08-491-988-7    | •                 |
| 11  | 50       | 57.1           | 435    | 7           | -08-491-98         | Ś                 |
| 12  | 36       | 55.4           | 249    | 4           | -08-9              | 74,               |
| 13  | _        | 54.7           | 244    | 7           | -08-553-497A-      | Ŋ                 |
| 14  | 23       | 54.4           | 288    | 4           | 19-423-4           | 38,               |
| 15  | 23       | 54.4           | 673    | 4           | -09-423-43         | 32,               |
| 16  | 22       | 54.4           | 246    | 7           | -553-4             | 24,               |
| 17  | 7        | ٠.<br>د        | 267    | 4           | -09-485-7          | 7                 |
| 18  | 711.5    | 53.5           | 541    | 7           | US-09-485-737B-85  | α                 |
|     | 7        | س              | 711    | ₩           | -09-485-7          | 9                 |
|     | 710      | 'n.            | 239    | m           | -08-279-772A-      | œ                 |
| 21  | 710      | 53.4           | 239    | 4           | -08-902-48         | 11,               |
|     | <b>.</b> | 53.4           | 599    | Н           | 3-1                | 3                 |
|     | 60       | ÷              | 244    | 7           | -08-553-4          | 22,               |
|     | 96       | ci             | 240    | -           | -488-113B-14       | 148               |
| 25  | 98       | •              | 240    | <del></del> | US-08-477-484B-148 | 148               |
|     | 698.5    | 52.6           | 240    | 7           | -08-646-360-14     | Sequence 148, App |
| 27  | 9        | ٠              | 240    | 4           | US-08-839-765-148  | 148               |

| Seguence 148, App<br>Seguence 2, Appli |                    | Sequence 16, Appl | Sequence 16, Appl | Sequence 79, Appl | Sequence 26, Appl |                  | 91,               |                   | 40,              | 44,              | 51,              | 8               |                 | Sequence 11, Appl | Sequence 11, Appl | Sequence 16, Appl |
|----------------------------------------|--------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-----------------|-----------------|-------------------|-------------------|-------------------|
| US-09-136-389-148<br>US-08-652-507-2   | US-08-646-265A-109 | US-08-661-052-16  | US-09-188-082-16  | US-08-918-148-79  | US-08-553-497A-26 | US-08-797-689-18 | US-09-485-737B-91 | US-08-553-497A-28 | US-09-184-658-40 | US-09-423-439-44 | US-09-423-439-51 | US-08-800-198-8 | US-09-296-595-8 | US-08-235-838-11  | US-08-465-473B-11 | US-08-235-838-16  |
| 40                                     | 4                  | 7                 | 4                 | 4                 | ~                 | 7                | 4                 | 7                 | ពា               | 7                | ₹                | C)              | m               | -                 | N                 | Н                 |
| 240                                    | 269                | 553               | 553               | 244               | 242               | 249              | 240               | 242               | 284              | 281              | 999              | 240             | 240             | 241               | 241               | 637               |
| 52.6<br>52.4                           | 52.3               |                   | 52.3              |                   | 52.2              | 52.2             | 51.2              | 50.9              | 50.9             | 50.4             | 50.4             | 50.2            | 50.2            | 50.0              | 50.0              | 50.0              |
| 698.5<br>696                           | 695                | 695               | 695               | 694               | 693,5             | 693.5            | 089               | 676.5             | 6.676.5          | 670              | 670              | 299             | 299             | 664               | 664               | 664               |
| 28<br>29                               | 30                 | 31                | 32                | 33                | 34                | 35               | 36                | 37                | 38               | 39               | 40               | 41              | 42              | 43                | 44                | 4.5               |

### ALIGNMENTS

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELEPHONE: 650/25-5416
TELEPHONE: 650/25-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear Sequence 9, Application US/09079029; Sequence 9, Application US/09079029; Patent No. 6342369; GENERAL INFORMATION; APPLICANT: Ashkenazi, Avi J. APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA US-09-079-029-9

US-09-079-029-9

Gaps 9 Length 309; Indels Ouery Match 75.0%; Score 997; DB 4; 1 Best Local Similarity 76.3%; Pred. No. 4.6e-75; Matches 190; Conservative 24; Mismatches 29;

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9 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGQGLEWMGWINPNSGGTNY 40 EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY ð g

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Run

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Sequence 39412, A Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 118537, Sequence 2, Appl Sequence 73, Appl Sequence 42, Appl Sequence 42, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 49, Appl Sequence 48, Appl Sequence 14, Appl Sequence 14, Appl Sequence 48, Appl
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!: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep: *

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!: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep: *

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|           | FAMILIES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 262;<br>9;                                | NSGG'<br>:-<br>GNGN'                                           | YMDV                                                           | ASWY<br>    <br> ASWY                                        | SSGN                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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                                                                              | Length<br>Indels                          | QLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPGOGLEWMGWINPNSGGTNY<br> | KFQGRVTMTRDTSIGTAYMELSRLSSDDTAVYYCAR-DRYYGSSAYHRGSYYMDVWGR<br> | LVTVSSGGGGGGGGGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK<br> | QAPVLVIYGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV<br> |
| 6 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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| 785-43<br>785-43<br>785-43<br>785-51<br>785-51<br>537-12805<br>6106-13<br>882-13<br>785-45<br>6106-19<br>882-19<br>785-52<br>785-52<br>1474-82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                              | 1.5; DB<br>1.3e-60<br>ches 1              | MYWVRQAF<br> :     <br>MHWVRQAF                                | YYCAR-DF                                                       | VALGOTVR<br>           <br>VALGOTVR                          | LTITGAQA<br>         <br>LTITGAQA                             |
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No. 1.3<br>Mismatches    | IGYY.<br>   <br>ISYA                                           | DTAV<br>    <br>DTAV                                           | PAVS                                                         | NTAS<br>     <br>NTAS                                         |
| US-10-039-<br>US-10-139-<br>US-10-139-<br>US-09-791-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-09-791-<br>US-09-791-<br>US-09-791-<br>US-09-791-<br>US-09-791-<br>US-09-959-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-<br>US-10-139-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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No. 1<br>8; Mismatch | KASGYTF<br>            <br>KASGYTF                             | LSRLSSDI<br>      :<br>LSSLRSEI                                | SELTOD                                                       | FSGSSSGI<br>FILLIT<br>FSGSSSGI                                |
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3,<br>39412<br>1 Homo sapiens<br>: Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 6<br>6<br>vati                            | KPGASVK<br>        <br>KPGASVK                                 | DTSIGTA<br>      <br>DTSASTA                                   | TGGGGSG<br>:      <br>SGGGGSG                                | NNRPSGI<br>        <br>                                       |
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NOS:<br>FATENTION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION:<br>APPLICATION 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Pred. No. 4.6e-59;
; Mismatches 30
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APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
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TITLE OF INVENTION: Antibodies Against Tun
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
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Best Local Similarity 83.5%;
Matches 208; Conservative 11
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SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 250
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US-09-791-537-1444
; Sequence 1444, Application
; GENERAL INFORMATION:
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US-10-151-882-20
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4.6e-59;
                                                     AL STRUCTURES THEREOF
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9; Mismatches
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Pred. No. 4
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TITLE OF INVENTION: Antibodies Against
FILE REFERENCE: PF554PCT
CURRENT APPLICATION NUMBER: PCT/US02/1
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 250
GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL
TITLE OF INVENTION: METHODS OF USE TH
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 121575
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application PC/TUS0216106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 GQAPVLVIYGKNNRPSGIPDRFSGSSG
                                                                                                                                                                                                                                                                                                  3 QVQLVQSGAEVKKPGASVKVSCKASGYT
                                                                                                                                                                                                                                                                                                                                       AQKFQGRVTMTRDTSIGTAYMELSRLSS
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                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-121575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  82.7%;
ilarity 85.5%;
Conservative
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llarity 83.5%;
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Best Local Similarity
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208; Conserv
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PCT-US02-16106-20
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Matches 208
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Sequence 2, Application US/09949039

Sequence 2, Application US/09949039

GENERAL INFORMATION:
APPLICANT: HAWLEY, STEPHEN B.

TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

FILE REFERENCE: 057220/1301

CURRENT APPLICATION NUMBER: US/09/949,039

CURRENT FILING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 290
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GENERAL INFORMATION:
APPLICANT: HAWLEY, STEPHEN B.
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.1
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                 TLVTVSSGGGGTGGGGGGGGGGSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKP
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 170; Conser
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LENGTH: 296
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US-09-949-039-2
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HEREOF
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No. 2.26
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEIF FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,53; CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 118537
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FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                     72.8%; Score 73.5%; Pred.
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US-09-791-537-118537
                                                                                                                       ; ORGANISM: synthetic US-09-791-537-1444
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Best Local Similarity
Matches 183; Conser
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236 GGGTKLTVL 244
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                                                                           SEQ ID NO 1444
LENGTH: 262
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                                                                                                                                                                                                             198 RQAPRLVVYGKNERPSGIPERFSGSTSGDTASLTISGLQAEDEADYYCHSRDSNADLVVF
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                                                                                 Length 296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Human Genome Sciences, Inc.

### TITLE OF INVENTION: Vascular Endothelial Growth Factor-2

### FILE REFERENCE: PF112P9PCT

### CURRENT APPLICATION NUMBER: PCT/US02/11474

### CURRENT FILING DATE: 2002-04-12

### PRIOR APPLICATION NUMBER: 60/283,385

### PRIOR APPLICATION NUMBER: 60/350,366

### PRIOR APPLICATION NUMBER: 60/350,366

### PRIOR FILING DATE: 2002-01-24

### NUMBER OF SEQ ID NOS: 85

### SOFTWARE: PatentIn version 3.1
                                                                                                             Indels
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            Artificial Sequence:
                                                                                                           32;
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Best Local Similarity 70.4%; Pred. No. 2.9e-48;
Matches 178; Conservative 25; Mismatches 44;
                                                                                core 906; DB 5;
red. No. 1.4e-48;
Mismatches 32
                                                                                 Score
Pred.
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       OTHER INFORMATION: Description of OTHER INFORMATION: acid sequence US-09-949-039-75
                                                                                                          37;
                                                                               Query Match
Best Local Similarity 68.3%;
Matches 170; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO 73
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo saplens
PCT-US02-11474-73
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258 GGGTKVTVL 266
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PCT-US02-11474-73
FEATURE
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GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAI

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/369,860

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/323,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 252;
                                                                                                                                                                              APPLICANT: Rosen, Craig, et al.
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P9
CURRENT APPLICATION NUMBER: US/10/120,414
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/283,385
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
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                                                                                                      RESULT 10
US-10-120-414-73
; Sequence 73, Application US/10120414
; GENERAL INFORMATION:
249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-414-73
237 HVVFGGGTKLTVL
                     --VFGGGTQLTVL
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Best Local Similarity
Matches 178; Conser
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LENGTH: 252
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No. 6e-47;
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28; Mismatches
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CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Antibodies that I
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
                                                                                                                                                                                                                                                                                                                        66.1%; Score 68.1%; Pred.
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                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.13
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 NHVVFGGGTKLTVL 249
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SOFTWARE: Patentin Ver. 3
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US-10-139-785-42
                                                                                                                                                           SEQ ID NO 42
LENGTH: 245
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GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAI

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT FILING DATE: 2002-05-07

CURRENT FILING DATE: 2002-04-05

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DATE: 2001-09-21

PRIOR PELING DATE: 2001-09-21

PRIOR PELING DATE: 2001-09-21

PRIOR PELING DATE: 2001-09-09

PRIOR PELING DATE: 2001-09-09

PRIOR PELING DATE: 2001-09-09

PRIOR PELING DATE: 2001-09-09

PRIOR APPLICATION NUMBER: 60/299, 473

PRIOR PELING DATE: 2001-06-04

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-06

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-06

PRIOR PELING DATE: 2001-06
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                                                                                                                                                                                                                                                                                               Length 245;
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                                                                                                                                                                                                                                                                                         Score 878.5; DB 6;
Pred. No. 6e-47;
3; Mismatches 38;
                                                                                     FEATURE:
CTHER INFORMATION: T1014A04 scFv US-10-139-785-42
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                                                                                                                                                                                                                                                                                                                                                                               28;
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.1%;
Matches 173; Conservative 28
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US-10-039-785-46
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--HRSNTF-DPWGQG
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SQKFHGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARQ---
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that ImmunosporTITLE OF INVENTION: Antibodies that ImmunosporTITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-00-09
PRIOR FILING DATE: 2001-00-09
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR APPLICATION NUMBER: 60/309,473
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 49
LENGTH: 245
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Sequence 49, Application US/10039785
GENERAL INFORMATION:
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US-10-039-785-49
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Matches 172; Conser
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                                    Gaps
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                                                                                  176 YQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSG
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                                                                                                                                  DDTAVYYCARDRYYGSSAYHRGSYYMDVWGRG
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                                     15;
    Length
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No. 2.5e-46;
  DB 6;
                                 38;
                   5e-46;
 e 868.5;
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ismatches
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FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/139,

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/369,860

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-04
   Score
Pred.
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TITLE OF INVENTION: Antibodies that
TITLE OF INVENTION: Receptors
                                                                  1 EVQLVQSGAEVKKPGASVKVSCKASGYTI
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172 FQQHPGKAPKLIISEVSKRPSGVPDRLS
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                                                                                  AOKFOGRVTMTRDTSIGTAYMELSRLSS
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  65.3%;
68.1%;
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PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
Query Match
Best Local Similarity 68.1
Matches 173; Conservative
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Best Local Similarity
Matches 173; Conser
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SOFTWARE: Pate
SEQ ID NO 46
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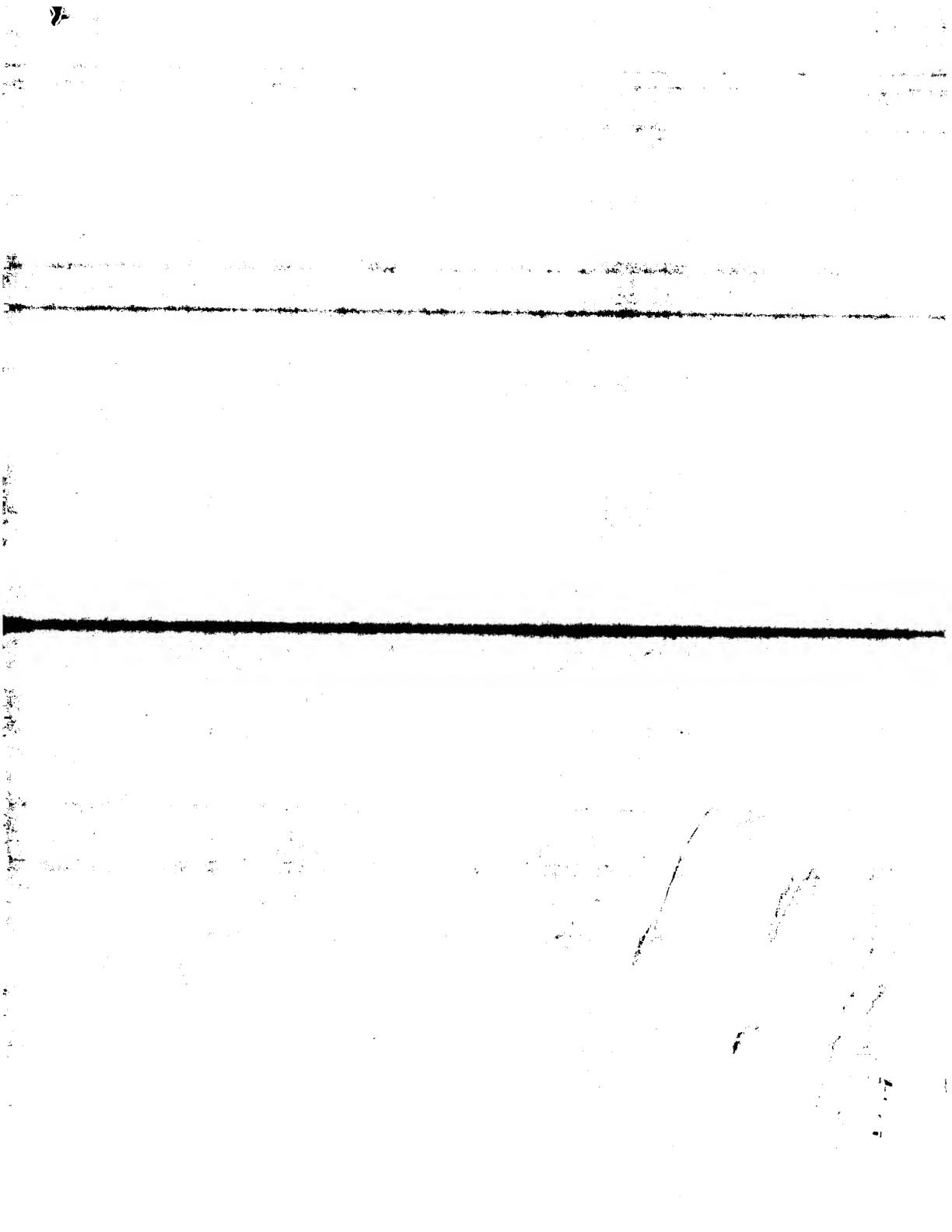
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172 YQQHPGKAPRLMISEVNKRPSGVPNRFSGSKSGNTASLTVSGLQADDEADYYCSSYAGS- 230 g

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90: Search completed: August 15, 2002, 16:27 Job time: 371 sec



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US-09-880-748-2021
Sequence 2021, Application US/09880748
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR RPELICATION NUMBER: 60/212,210
PRIOR RPELICATION NUMBER: 60/212,210
PRIOR PELING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-26
SOFTWARE: PATENTION NUMBER: 60/293,499
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2021
LENGTH: 242
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Best Local Similarity 89.6%; Pred. No. 8.8e-98;
Matches 223; Conservative 8; Mismatches 10; Indels 8
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; ORGANISM: Homo sapiens
US-09-880-748-2021
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Search completed: August 15, 2002, 16:34:04 Job time: 764 sec

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Pred. No. 3.5e-98;
8; Mismatches 10;
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US-09-880-748-2014

Sequence 2014, Application US/09880748

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Imm
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,7

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-017

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VEY. 2.0
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 2014
LENGTH: 243
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Best Local Similarity 90.0%;
Matches 224; Conservative 8
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; ORGANISM: Homo sapiens
PCT-US01-19110-2014
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US-09-880-748-2014
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LENGTH: 243
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Sequence 2021, Application PC/TUS0119110

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy;

FILE REFERENCE: PF523PCT

CURRENT APPLICATION NUMBER: PCT/US01/19110

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET. 2.0
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Pred. No. 8.8e-98;
8; Mismatches 10;
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Best Local Similarity 89.6%;
Matches 223; Conservative
Conservative
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PCT-US01-19110-2021
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PCT-US01-19110-2021
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1181.5; DB No. 3.5e-98;

Score Pred.

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Query Match Best Local Similarity

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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2.8e-98;
8; Mismatches 8;
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Conservative
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Best Local Similarity 90.0%;
Matches 224; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1722
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Best Local Simi
Matches 228;
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LENGTH: 241
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GQAPVLVIYGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVF
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PCT-US01-19110-2014
; Sequence 2014, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS;
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2008

LENGTH: 241
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US-09-880-748-2008
; Sequence 2008, Application US/09880748
; GENERAL INFORMATION:
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Best Local Similarity 90.0%;
Matches 224; Conservative
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US-09-880-748-2008
                                                                                                   GGGTKLTVL 249
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            DB 22;
1.1e-98;
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US-09-880-748-2046

Sequence 2046, Application US/09880748

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immr
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,7

CURRENT APPLICATION NUMBER: US/09/880,7

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENT VEF. 2.0
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Best Local Similarity 90.3%; Pred.
Matches 224; Conservative 7; Mis
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; ORGANISM: Homo sapiens
US-09-880-748-2046
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PCT-US01-19110-1722
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US-09-880-748-1722

Sequence 1722, Application US/09880748

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLY;

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR PELICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-15

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PALENTIN VET. 2.0

SEQ ID NO 1722

LENGTH: 250
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bin;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1722
LENGTH: 250
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Pred. No. 1.1e-98;
6; Mismatches 13;
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Best Local Similarity 90.8%;
Matches 228; Conservative
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PCT-US01-19110-1722
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bing FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379
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Pred. No. 7.3e-99;
7; Mismatches 9;
                                                                                       Sequence 2106, Application PC/TUS0119110
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immuno;
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/216,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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Best Local Similarity 90.4%;
Matches 225; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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234 GGGTKLTVL 242
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                                                              RESULT 4
PCT-US01-19110-2106
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US-09-880-748-2106
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Sequence 2046, Application PC/TUS0119110

GBNERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523PCT

CURRENT APPLICATION NUMBER: PCT/US01/19110

CURRENT FILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

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WINDER OF SEC. IT NACE: 2001-05-25
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Pred. No. 1,1e-98;
'; Mismatches 9;
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2106
LENGTH: 242
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90.3%;
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1larity 90.4%;
Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2046
LENGTH: 242
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                                       PRIOR FILING DATE: 2001-0;
NUMBER OF SEQ ID NOS: 323;
SOFTWARE: Patentin Ver. 2;
SEQ ID NO 2106;
LENGTH: 242;
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2106
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Best Local Similarity
Matches 225; Conser
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ORGANISM: HOMO (USO1-19110-2046
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Imm
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2107
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
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Amino Acid
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Matches 249; Conser
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ORGANISM: Homo :
PCT-US01-19110-2107
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PCT-US01-19110-2107
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                                                                                                                                                                                                                                                                                       RESULT 3
US-09-880-748-2107
Sequence 2107, Application US/09880748
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Binc CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET. 2.0
LENGTH: 243
TYPE: PRI
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Pred. No. 4.4e-99;
7; Mismatches 9; 1
Pred. No. 4.4e-99;
; Mismatches 9;
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Best Local Similarity 90.8%;
Matches 226; Conservative
 90.8%;
             Conservative
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                                                                                                                                                                                                                                                                  GGGTKLTVL 249
                                                                                                                                                                                                                                                    GGGTKLTVL 249
Best Local Similarity
Matches 226; Conser
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Length 243;

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DB

1191.5;

Score

89.78;

Query Metch

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4.5
Compugen Ltd
version
- 2000
GenCore
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protein search, using sw model OM protein

٠. August 15, 2002, 16:34:03 Run on:

updates/sec Search time 410.32 Seconds (without alignments) 213.597 Million cell upda

.. SRDSSGNHVVFGGGTKLTVL US-08-779-457-48 1329 1 EVQLVQSGAEVKKPGASVKV. score: Title: Perfect so Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 3502263 segs, 351980561 Searched:

Total number of hits satisfying chosen parameters

residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summar

Database

Pending\_Patents\_AA\_Main:\*

1: \( \cgn2\_6\) \( \text{ptodata} \) \( \text{paa} \) \( \text{VCOMB.pep:\*} \) \( \cgn2\_6\) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO6\_COMB.pep:\*} \) \( \cgn2\_6\) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO8\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO9\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO9\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO9\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Paa} \) \( \text{VSO9\_1\_COMB.pep:\*} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Sgn2\_6} \) \( \text{ptodata} \) \( \text{Sgn2\_6} \) \( \text{Sgn2\_6} \) \( \text{Sgn2\_6} \) \( \text{Ptodata} \) \( \text{Sgn2\_6} 

predicted by chance to have a score of the result being printed, total score distribution. Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

## SUMMA

| Result<br>No. | Score  | %<br>Ouery<br>Match | %<br>Query<br>ore Match Length DB I | DB | ID                  | Description       |
|---------------|--------|---------------------|-------------------------------------|----|---------------------|-------------------|
| 7             | 1329   | 100.0               | 249                                 | 11 | 11 US-08-779-457-48 | Sequence 48, Appl |
| 7             | 1191.5 | 89.7                | 243                                 | -  | PCT-US01-19110-2107 | Sequence 2107, Ap |
| m             | 1191.5 |                     | 243                                 | 22 | US-09-880-748-2107  | Sequence 2107, Ap |
| 4             | 1189   |                     | 242                                 | -  | PCT-US01-19110-2106 | Sequence 2106, Ap |
| ហ             | 1189   |                     | 247                                 | 22 | US-09-880-748-2106  | Sequence 2106, Ap |
| 9             | 1187   |                     | 242                                 | Н  | PCT-US01-19110-2046 | Sequence 2046, Ap |
| ^             | 1187   |                     | 242                                 | 22 | US-09-880-748-2046  | Sequence 2046, Ap |

Sequence 2008, Ap Sequence 2014, Ap Sequence 2011, Ap Sequence 2021, Ap Sequence 2021, Ap Sequence 1723, Ap Sequence 2032, Ap Sequence 2031, Ap Sequence 2031, Ap Sequence 1721, Ap Sequence 1721, Ap Sequence 1729, Ap Sequence 2033, Ap Sequence 927, App Sequence 927, App Sequence 948, App Sequence 948, App Sequence 948, App Sequence 967, App Sequence 1947, Ap Sequence 1947, Ap Sequence 1638, Ap Sequence 1638, At Sequence 1730, Ap Sequence 1730, Ap Sequence 1722, Sequence 172: Sequence 2008 22 US-09-08 0-748-1722 US-09-08 0-748-1722 US-09-08 0-748-2008 US-09-08 0-748-2014 US-09-08 0-748-2014 US-09-08 0-748-2014 US-09-08 0-748-2014 US-09-08 0-748-2011 US-09-08 0-748-2011 US-09-08 0-748-1723 US-09-08 0-748-1723 US-09-08 0-748-1907 US-09-08 0-748-1907 US-09-08 0-748-1907 US-09-08 0-748-1907 US-09-08 0-748-1919 US-09-08 0-748-1947 US-09-08 0-748-1947 US-09-08 0-748-1947 US-09-08 0-748-1947 US-09-08 0-748-1947 US-09-08 0-748-1947 PCT-US01-19110-1538 2 US-09-880-748-1638 PCT-US01-19110-1730 2 US-09-880-748-1730 1187.5 11182.5 11182.5 11182.5 11181.7 11177.7 11170.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11162.5 11163.5 11143.5 11145.5 11136.5 11136.5 

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RESULT 1
US-08-779-457-48

| Sequence 48, Application US/08779457
| GENERAL INFORMATION:
| APPLICANT: Carter, Paul J. |
| APPLICANT: Kyung, Jin Kim |
| APPLICANT: Matthews, William |
| APPLICANT: Rodrigues, Maria L. |
| TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Genentech, Inc. |
| STREET: Genentech, Inc. |
| STATE: California |
| COUNTRY: USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21P: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/779,457 FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
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|-----------------------------------------------------------------------------------------------|-------------------------|--------------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------|-------------------------------------------------------------|----------------------------------------------|
| 31; Gaps                                                                                      | ANY 60                  | 1<br>ryy 79                                                        | -VW 11                                                         | <br>                                                  | 172                                                         | 170                                          |
| 31;                                                                                           | PIFGT                   | <br>PGSGS1                                                         | <u>0</u> -                                                     | ↓<br>DYDWF#                                           | DVGGY                                                       | -VKGY                                        |
| Indels                                                                                        | SLEWMGGII               | SLEWIGKIG                                                          | PATSLEGE                                                       | RSGY                                                  | TISCTGTSS                                                   | rece                                         |
| 38;                                                                                           | DAPGKC                  | QRPGQC                                                             | DRVVVE                                                         |                                                       | PGQSIT                                                      | IGSSVI                                       |
| best bota Similality 40.3%; Fied, NO. 1.38-21;<br>Matches 83; Conservative 25; Mismatches 38; | ESLKISCOGSGFTFSSYKMNWVR | 20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYXINWVKQRPGQGLEWIGKIGPGSGSTYY 79 | 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVW 115 | NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYW 128 | GTTVTVSSGGGGGGGGGGGGGGGGGVLTQPASVSGSPGQSITISCTGTSSDVGGY 172 | GTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGY 170 |
| 83; Conserva                                                                                  | EVQLVQSGAEVKKPG         | OVQLKQSGAELVKPG                                                    | AQKFQGRVTITADES                                                | NEKFKGKATLTADKS                                       | GOGTTVTVSSGGGGS                                             | GOGTLVTVS                                    |
| ches                                                                                          | <b>T</b>                | 20                                                                 | 61                                                             | 80                                                    | 116                                                         | 129                                          |
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Search completed: August 15, 2002, 16:35:37 Job time: 797 sec

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Query Match
Best Local S
Matches 78
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                                              EDUCINCE FROM N.A.

TISSUE-GASTRIC MUCOSA;

TISSUE-GASTRIC MUCOSA;

Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,

Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,

Kawakami B., Nagai K., Isogai T., Sugano S.;

"NEDo human cDNA sequencing project.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK058027; BAB71633.1;

SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VTVSSGGGGGGGGGGGGGGGGGGGVLTQPASV-SGSPGQSITISCTGTSSDVGGYNYVSWYQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEP-----LSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVHLVQSGAELKMPGSSVKVSCKASANMFRSYAFTWVRQAPGQGLQWMGGIIPNFGAPNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLYQSGAEVKKPGESLKISCQGSGFTFSSYKMNWVRQAPGKGLEWMGGIIPIFGTANY 60
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MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ASPISPKVFPLSLCSTQPDGNVVIACL----VQGF----FP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IGG VH PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 102; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
NCBI_TaxID=9606;
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01-NOV-1999
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09Y298
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CTRAIN=C57BL/6J; TISSUE=PANCREAS;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Batsubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Haynschizzei V.
                                                                                                                                                                                                                                     IGH-1 OR 1810060009RIK.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;
                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR003599; Ig.
InterPro; IPR003590; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003596; Ig_WHC.
                                                           ..
89
Length 150;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edu: PF00047; ig: 4.

SMART; SM00409; IG: 2.

SMART; SM00406; IGv: 1.

SMART; SM00410; IG_like; 1.

SMART; SM00410; IG_like; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
Score 388; DB 4;
Pred. No. 2.2e-22;
15; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA
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29.8%;
llarity 62.4%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
1810060009RIK PROTEIN.
                               Local Similarity
nes 78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                  121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                            132 VTVSS 136
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DB 11; Length 473;

Score 385.5;

29.78;

us-08-779-457-49.rspt

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trematoda; Digenea; Strigeidida Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GYZ2
09GYZ2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain
NP30 of
AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARGY----SSSWDDAFDIWGQGTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCAR---DRVVVPATSLRGGMDVWGQ
                                                                     | | | | : : |
ENSPSDTSSVAVGCLAQDFLPDSITFSWKY
                                                                                                                                                                                                                                         245 VIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQV
                                                                                                                                                                                                                                                                                                                    : :|| : | | : | | | : | | | OAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAVYYCARYYDDHYC-----LDYWGO
                                                                                                                                                                  185 KNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNVPLP
                                                                                                                                                                                                              --EGSKRPSGVSN---
                                                                                                                                                                                                                                                                                              -----GLQAEDEADYYCSSYTTRSTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Song X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy cha variable region gene of monoclonal anti-idiotypic antibody NP3 Schistosoma japonicum.";
Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
REMBL; AF282622; AAG01452.1; -..
RINGEPPO; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003506; Ig_NEC.
InterPro; IPR003506; Ig_NEC.
InterPro; IPR003506; Ig_NEC.
RINGEPPO; IPR003596; Ig_V.
REMBRT; SM00409; IG; I.
SMART; SM00400; IG_like; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119
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                                           VTVSSGGGGGGGGGGGGGQSVLTQPASVSGSPG--QSITISCTG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core 399; DB 5;
red. No. 2.4e-23;
Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BA89
                                                                                  ----GSASAPTLFPLVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.7%; Score 61.7%; Pred.
                                                                                                                          -TSSDVG------GYNYVSWYQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                             RFSGSKSGS----TASLTIS----
                                                                                                                                                                                                                                                                                                                                                                            ----GGTKLTVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                  365 FAIPPSFASIFLTKSTKLTCL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
13567 MW;
                                                                                                                                                                                                           ----KAPKLMIY-----
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119 AA;
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 GTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6182;
                                                                   136 VTVSS---
                                                                                                                                                                                                                                                                                                                                                                           241 FG----
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NON_TER
SEQUENCE
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09GY22
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 VSWYQQHPGKAPKLMIYEGSKRPSGVSNR-----FSGSKSGSTASLTISGLQ--AEDE
                                                                                                                                             Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096DK0
096DK0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN
ALPHAI H,MYELOMA.
               09BRV0;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 397.5; DB 4;
Pred. No. 1.7e-22;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; 0A9BF4
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6%; Scu
40.4%; Pre
                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMEMBL; BC005951; AAH05951.1; -.
HSSP; P01789; 1MCP.
INTERPRO; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ADYYCSSYTTRSTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 VTCHVKHYTNPSQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            TISSUE-PROSTATE;
Q9BRV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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